Sequence 11, Appl
Sequence 3, Appli
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 3511, Ap
Sequence 3511, Ap
Sequence 181, Ap
Sequence 181, Appl
Sequence 181, Appl
Sequence 187, Appl
Sequence 44, Appl

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Post-processing: Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-854-585-2
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US-08-854-585-2
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                                              Matches
                                                     Query Match
Best Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
FILING DATE:
                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tonks, Nicholas K. and TITLE OF INVENTION: Density Enhanc NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             STREET: 233 SOCITY: Chicago STATE: Illinoi: COUNTRY: United
          324 QSRDTEVL 331
                                                     Local Similarity
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                          1 QSRDTEVL 8
                                                                                                                            LENGTH:
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United States of
                                                                                                                            1337 amino acids
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233 South Wacker Drive, Suite 6300
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US-09-157-021-31

US-09-156-842-31

US-08-326-117B-2

US-08-962-129-2

US-08-962-284-4

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US-07-925-695-8

US-07-925-695-8

US-07-187-859-3511

US-09-187-859-3514

US-09-187-859-3514

US-09-188-579-26

US-09-188-579-26
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                                                     Score 8;
Pred. No.
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                                             Mismatches
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Phosphatase

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DB 3; 0.061;

Length 1337 Indels

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Gaps

0;

Minimum

Word size

Searched:

Maximum

DB

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Database :

Title: Perfect score:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US95-05512-2
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                                                                                                                                                                                                                                                                                                                                                   Patent No. 5981277
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: BORUN, MIChael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
    ZIP: 10010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY
TITLE OF INVENTION: IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
                                                                                                                                                                                               NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino aci
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OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                 COUNTRY:
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Pred. No. 0.061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08318837 Patent No. 5981277
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                           CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 13-OCT-1994
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE, APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-APR-1992 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                          CITY: NEW YORK
STATE: NEW YORK
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CLASSIFICATION:
APPLICATION NUMBER: 92.401.231.3 FILING DATE: 30-APR-1992
                                                                                                                                                                    SOFTWARE: ASCII
                                                                                                                                                                                                                                                                  COUNTRY:
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nes 5; Conserv
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TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 28-APR-1993
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linear
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PU5-1.8, THP-1
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internal
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100.0%; Pred. No.
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Best Local Similarity
Watches 5; Conserve
                                                                                                          US-08-326-117B-14
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                                             Query Match
Best Local
                                Matches
                                                                                                                                                                                  TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BULLA, LEE A. APPLICANT: JI, TAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                  TELEPHONE: (202) 887-0763
                                                                                                                       LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                            NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 7112-0037.00
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/326,117B FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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5. 5693491
                              Similarity 5; Conserv
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2000 Pennsylvania Ave. N.W.
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                         62.5%; Score 5; DB:
llarity 100.0%; Pred. No. 23
Conservative 0; Mismatches
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llarity 100.0%; Pred. No. 4.:
Conservative 0; Mismatches
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                                                          Length 122;
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RESULT 7
US-08-928-443-1
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                                                                                                                                                             Sequence 1, Application US/08928443 Patent No. 5795724
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Best Local
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                                                                  GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN N-ACETYL TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
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APPLICANT: JI, TAE
TITLE OF INVENTION: T
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/326,117
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDLING TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
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ADDRESSEE: MORRISON & FOERSTER
                                    CORRESPONDENCE ADDRESS
                                                         NUMBER OF SEQUENCES:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                Local Similarity 100 tes 5; Conservative
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REFERENCE/DOCKET NUMBER: 7112-0037.00
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CLASSIFICATION:
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CITY: Washington
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ZIP: 20006-1812
                 ADDRESSEE:
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3174 Porter Drive
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100.0%; Pred. No.
Live 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                Mismatches
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Matches
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,443
FILING DATE: HERBUITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09129055 Patent No. 6017744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN N-ACETYL TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 178 amino acids
                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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TELEPHONE: 650-845-4166
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS ADDRESSEE: Incyte Pl
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LIBRARY: BRAITUT02
CLONE: 761783
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NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/928,443
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                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                           ZIP: 94304
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                               CITY: Palo Alto
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Local Similarity 100.0%; Pred. No. 33
Nes 5; Conservative 0; Mismatches
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STRANDEDNESS: sir
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ZIP: 94304
FILING DATE:
                                                    CLASSIFICATION:
                                                                   FILING DATE:
                                                                                     APPLICATION NUMBER: US/09/129,055
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US-08-318-837-7
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE
TITLE OF INVENTION: IMMUNOLOGY
                               TELEFAX: (212) 661-80 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 178 amino acid
                                                              REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
                                                                                                                                                     APPLICATION NUMBER: PCT/EP 93/010
FILING DATE: 28 APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92.401.231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 15m FC COPERATING SYSTEM:
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MEDIUM TYPE: Floppy disk
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TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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LIBRARY: br...
761783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 SRDTE 161
                                                                                                                  NAME: CHARLES A. MUSERLIAN REGISTRATION NUMBER: 19,683
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/318,837 FILING DATE: 13-OCT-1994
                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: NEW YORK
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CENGTH:
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linear
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661-8002
NO: 7:
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100.0%; Pred. No.
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RESULT
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                                                                                                                    Matches
                                                                                                                  Best Local Similarity
Matches 5; Conserv
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Best Local Similarity 100
Matches 5; Conservative
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92.401.231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.007
TELECOMMUNICATION INFORMATION:
THE TENTIONE: /373 / 641.8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 661-80 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY
TITLE OF INVENTION: IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE, APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
                                                 193 DTEVL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 DTEVL 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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11
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                                                                                 4 DTEVL 8
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                                                                                                                                                                                                                                                    amino acid
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100.0%; Pr
                                                                                                                 62.5%; Score 5; DB;
100.0%; Pred. No. 56;
tive 0; Mismatches
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; Pred. No.
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                                                                                                                                    DB 2;
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                                                                                                                                                 Length 311;
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US-08-356-405-2
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Best Local :
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                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                             APPLICANT: Hen, Rene
APPLICANT: Plassat, Jean-Luc
TITLE OF INVENTION: Polypepti
TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Construction and USe of Synthetic TITLE OF INVENTION: Constructs Encoding Syndecan NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Mert
APPLICANT: Kato, Masato
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 17-JUN-1993 CLASSIFICATION: 435
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nes 5; Conserv
COUNTRY: USA
ZIP: 19426-0107
                                 STATE:
                                                                STREET:
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                                                                ADDRESSEE: Rhone-Poulenc Rorer STREET: 500 Arcola Road, 3C43
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internal
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100.0%; Pr/
0;
                                                                                                                                              Polypeptides Having Serotonin Receptor Activity (5HT5A), Nucleic Acids Coding for These
                                                                                                                 Polypeptides and Uses Thereoi
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Pred. No.
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COMPUTER READABLE FORM:

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RESULT 13
US-08-806-263-2
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APPLICANT: Sathe, Ganesh
APPLICANT: Van Horn, Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/0
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/ACENT INFORMATION:
NAME: Smith, Julie K
RECISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: EX92004-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/O
FILING DATE:
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                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
NAME: Han, William T
REGISTATE NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH:
TELECOMMUNICATION INFORMATION:
                                                                                                                              APPLICATION NUMBER: US/0: FILING DATE: 24-FEB-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
                                                      ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Van Horn, Stephanie
TITLE OF INVENTION: cDNA Clone HDPBI30 That Encodes
TITLE OF INVENTION: A No. 6221627el Human 7-Transmembrane Receptor
                                                                                                                                                                                                                                                                                                                                                                              STREET:
CITY: F
                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19406
                                                                                           FILING DATE:
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nes 5; Conserva
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                               APPLICATION NUMBER:
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TD NO: 2:
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100.0%; Pred. No.
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                                                              ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-969-815-4
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US-08-969-815-4
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Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATTORNEY_AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Witte, Owen N.
APPLICANT: Weng, Zhigang
TITLE OF INVENTION: IDENTIFICATION OF A G PROTEIN-COUPLED
TITLE OF INVENTION: RECEPTOR TRANSCRIPTIONALLY REGULATED BY PROTEIN
TITLE OF INVENTION: TYROSINE KINASE SIGNALING IN HEMATOPOIETIC CELLS
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: UCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEPHAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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62.5%;
100.0%;
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100.0%; Pred. No.
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 Score 5;
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                Length 380;
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; MOLECULE TYPE: protein ; FRAGMENT TYPE: internal US-09-120-025-4
Search completed: August 31, 2002, 12:20:20 Job time: 135 sec
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US-09-120-025-4
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SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                           Query Match 62.5%; Score 5; DB 4; Best Local Similarity 100.0%; Pred. No. 67; Matches 5; Conservative 0; Mismatches
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/969,815
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REGISTRATION INDMER: UCLA015.001
TELECOMMUNICATION INDMER: UCLA015.001
TELEPHONE: 619-235-050
TELEPAX: 619-235-0176
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APPLICANT: Witte, Owen N.
TITLE OF INVENTION: TRANSCRIPTIONALLY REGULATED G PROTEIN-COUPLED TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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341 SRDTE 345
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STATE: CA
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1SPD_CHLTR
PYRE_KIULA
VMFC_BACSU
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RL5_DUNSA
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RL5_DUNSA
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Y4-56_MYCGE
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Q9u156 homo sapien
P04490 human adeno
 P08586 va
P20539 va
P80017 ca
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EMBL; U10886; AAB3687.1; EMBL; D37781; BAA07035.1; HSSP; P18052; 1YFO. MIM; 600925; InterPro; IPR0003961; FN_III. InterPro; IPR000387; TYR_phosphatase. InterPro; IPR000242; Tyr_prot_phphtase. Pfam; PF00041; fn3; 5. Pfam; PF00102; Y_phosphatase; 1.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	tyrosine + phosphate.  tyrosine + phosphate.  subcellular LOCATION: Type I membrane protein.  - PTM: N - AND O-GLYCOSYLATED.  - SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAI  - SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  - DATABBASE: NAME-PROW; NOTE-CD guide CD148 entry;  WWWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".	MEDLINE-95086212; PubMed-7994032; MEDLINE-95086212; PubMed-7994032; MeDLINE-95086212; PubMed-7994032; Medline-95086212; PubMed-7994032; Molecular cloning, characterization, and chromosomal localization of "Molecular cloning, characterization, and chromosomal localization of a novel protein-tyrosine phosphatase, HPTP eta."; Blood 84:4186-4194(1994)	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-95024024; PubMed-7937872; Oestman A., Yang Q., Tonks N.K.; "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced with increasing cell density."; Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).	PTERO OR DEPI. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	UMAN TPJ_I 1291 1291 1-NOV 1-NOV 1-MAI 1-MAI

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PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
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SMART; SM00194; PTPC;
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Pred. No.
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MEDLINE-95305574; PubMed-7786018;
MEDLINE-95305574; PubMed-7786018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arch. Biochem. Biophys. 357:27-36(1998).
-!- FUNCTION: HIGH ACTIVITY FOR THE HYDROXYLATION IMIPRAMINE; LOW ACTIVITY ON DEBRISOQUINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sakamoto K., Kirita S., Baba T., Nakamur Takanaka A., Matsubara T.; "A new cytochrome P450 form belonging to microsomes: purification, cDNA cloning,
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Rukarvota; Metazoa; Chordata;
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HSSP; P00179; IDT6.
InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450;
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J. Biochem. 123:162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; NCBI_TaxID-9615;
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Cytochrome P450 2D15 (EC 1.14.14.1) (CYPIID15) (P450 DUT2).
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Tweedie D.J.;
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MEDLINE=98389575; PubMed=9721180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98162950; PubMed=9504424;
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381
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SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

TISSUE SPECIFICITY: LIVER. ALSO DETECTED IN SEVERAL OTHER TISSUES.

SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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ilarity 100.0%;
Conservative
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Pred. No.
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome P450 2D16 (EC 1.14.14.1) (CYPIID16).
CYP2D16.
                                                                                                                                                                                                                                 EMBL; U21486; AAA68479.1; -. EMBL; AF020345; AAB94568.1;
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-HARTLEY WHITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang Q., Voigt J.M., Colby H.D.;
"Molecular cloning and sequencing of a guinea pig cytochrome (CYE2D16): high level expression in adrenal microsomes.";
Biochem. Biophys. Res. Commun. 209:1149-1156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN=13; TISSUE=Adrenal cortex; MEDLINE=95251703; PubMed=7733969;
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382
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                                                                                                                                                                                                                                                                                                                                                                              ACIDS, AND XENOBIOTICS.

CATALYTIC ACTIVITY: H reduced flavoprotein + O(2) oxidized flavoprotein + H(2)O.

SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic re-
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE:
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01-AUG-1992 (Rel. 23, Las
Early ElB 9 kDa protein.
Human adenovirus type 7.
Viruses; dsDNA viruses, r
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E1B9_ADE07
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"Functional prediction of the coding sequences of 50 new by analysis of CDNA clones from human fetal liver.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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Q9UI56;
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Dijkema R., Dekker B.M.M., van Or
"Gene organization of the transfo
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        EMBL; X03000;
                              entities requires a license agreement (s or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa;
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01-FEB-1991 (Rel. 1:
16-OCT-2001 (Rel. 4:
Late protein H7.
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Rosel J.L., Earl P.L., Weir J.P., Moss B.;
Rosel J.L., Earl P.L., Weir J.P., Moss B.;
Roserved TAAATG sequence at the transcriptional and translational initiation sites of vaccinia virus late genes deduced by structural and functional analysis of the HindIII H genome fragment.";
J. Virol. 60:436-449(1986).
  NCBI_TaxID=10249
               Orthopoxvirus.
                       Vaccinia virus (strain Copenhagen)
Viruses; dsDNA viruses, no RNA sta
                                                                                                                                                                                                                                                                                               Late protein.
                                                                                                                                                                                                                                                                                                                  EMBL; M13209; AAB59843.1;
PIR; H24481; QQVZH8.
                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orthopoxvirus
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SEQUENCE 88
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5. 22;
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Best Local
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01-MAY-1991 (Rel. 18, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS), Mitchell D.T., Ernst S.R., Hackert M.L. "X-ray structure determination of a dimarenicola.";
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                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91265540; PubMed=2049384; Mauri F., Omnaas J., Davidson L., Whitfill C., "Amino acid sequence of a globin from the sea (Molpadia) arenicola.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goebel S.J., Johnson Paoletti E.;
                                                                                                                                                                                                            Acta Crystallogr. D 51:760-766(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caudina arenicola (Sea cucumber) (Molpadia arenicola).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Appendix to 'The complete DNA sequence of vaccinia virus'."; virology 179:517-563(1990).
                       PIR; S15979; S15979.
PDB; 1HLM; 07-FEB-95.
InterPro; IPR000971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Coelomic fluid;
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MEDLINE=91021027; PubMed=2219722;
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Paolettí E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete DNA sequence of vaccinia virology 179:247-266(1990).
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                                                                                                                    HEMOGLOBIN CHAINS LABELED SIMILARITY: STRONG, TO C.1
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                       Biophys. Acta 1078:63-67(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=2049384;
J., Davidson L.,
                                                                                                                                                                  CAUDINA ARENICOLA COELOMOCYTES
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cucumber Caudina
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Best Local S
Matches
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MEDLINE=94040790; PubMed=8224889;
Gu Z.-M., Martindale D.W., Lee B.H.;
Gu E.33:147-147(1993).

-i- CATALYTIC ACTIVITY: 5-phospho-beta-D-ribosylamine + diphosphate
-i- CATALYTIC ACTIVITY: 5-phospho-alpha-D-ribose 1-diphosphate
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P35853;
01-JUN-1994
01-FEB-1996
InterPro; IPR000583; GATASe_2.
InterPro; IPR002375; Pur_pyr_pr_transf.
Pfam; PF00310; GATASe_2; IT
PROSITE; PS00103; PUR_PYR_PR_TRANSFER; PARTIAL.
PROSITE; PS00443; GATASE_TYPE_II; 1.
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                     EMBL; M85265; AAC36948.1; PIR; PC1136; PC1136.
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Gu Z.-M., Martindale D.W., Lee B.H.;
"Isolation and complete sequence of t
synthase II in Lactobacillus casei.";
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Heme; Oxygen trans
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                                                                                                                                                   PC1136; PC1136.
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                                                                                                         P00497; 1A
S; C44.001;
                                                                                                                                                                                                               an email to license@isb-sib.ch).
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IRON (HEME PROXIMAL LIGAND).
ATQ -> QAT (IN REF. 1).
T -> W (IN REF. 1).
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                                                                                                                             InterPro; IPR002565; Orbi_NS3.
Pfam; PF01616; Orbi_NS3; 1.
ProDom; PD003183; Orbi_NS3; 1.
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15-DEC-1998
16-OCT-2001
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Q64904;
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SEQUENCE
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ACT_SITE
                                                                                         Nonstructural protein.
CHAIN 1 217
CHAIN 12 217
CHAIN 12 217
SEQUENCE 217 AA; 23663
                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                   "Phylogenetic analysis of segment 10 from African horses and cognate genes from other orbiviruses."; Virus Res. 33:157-165(194).
-1- FUNCTION: MAY PLAY A ROLE IN THE RELEASE OF VIRIONS
                                                                                                                                                                                                                                                                                                                                                                                                 African horse sickness virus 4 (AHSV-4) (African
                                                                                                                                                                                                                                                                                                                                                                                                              S10
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                                                                                                                                                               EMBL; U02712; AAA21527.1;
                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE REOVIRUSES NS3 FAMILY.
                                                                                                                                                                                                                                                                                                                             de Sa R., Zellner M., Grubman M.J.;
                                                                                                                                                                                                                                                                                                                                       MEDLINE=95066364;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Nonstructural
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DTEVL
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21144
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1 BY SIMILARITY.
94 AMIDOPHOSPHORIBOSYLTRANSFERASE.
12 GATASE (INVOLVED IN SUBSTRATE B
CATALYSIS) (BY SIMILARITY).
                                                62.5%;
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Last annotation updat
NS3 [Contains: Nonstr
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Pred. No.
                                                                                         NONSTRUCTURAL PROTEIN NS3.
NONSTRUCTURAL PROTEIN NS3A.
; 4CFD0C4E0B9612F4 CRC64;
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32;
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35;
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RESULT 11 ISPD\_CHLTR ID ISPD\_C AC 084468

ISPD\_CHLTR O84468;

STANDARD;

219

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RESULT 12
PYRE_KLULA
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Matches 5
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                                                                                                                                                             PYRE_KLULA STANDARD; PRT; 226 AA (0.13474; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation updat (protate phosphoribosyltransferase (EC 2.4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis. Bacteria; Chlamydiales;
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01-MAR-2002 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
01-MAR-2002 (Rel.
                  Bai X., Larsen M., Meinhardt Submitted (SEP-1997) to the
                                               STRAIN=CBS 683;
                                                                                                       Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; Saccharomyc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stephens R.S., Kalman S., Lammel C.J., Fan J., Mitchell W.P., Olinger L., Tatusov R.L., Zhao C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-D/UW-3/CX;
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                                                             SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01295; ISPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99000809; PubMed=9784136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol. PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                 DTEVL 159
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                                                                                                       Saccharomycetaceae;
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                        Score 5; DB 1; Pred. No. 36; 0; Mismatches
                                                                                                                       Saccharomycotina; Saccharomycetes
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2.4.2.10)
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RESULT 13
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                                                                       EMBL; X73124; CAA51637.1;
EMBL; Z99123; CAB15800.1;
PIR; S39736; S39736
SubtiList; BG10627; YwfC.
                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonz
Hullo M.F., Ionescu M., Lubochinsky B., Marcelino
Presecan E., Santana M., Schneider E., Schweizer J
Rapoport G., Danchin A.;
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InterPro; IPR002375; Pur_pyr_pr_transf.
InterPro; IPR002375; Pur_pyr_pr_transf.
InterPro; IPR002375; Pur_pyr_pr_transf.
IPS00103; Pur_pyr_PR_TRANSFER; 1.
INTERPORT INTERPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40,
Hypothetical 26.8 kDa
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NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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PATHWAY: FIFTH STEP IN PYRIMIDINE BIOSYNTHESIS
SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
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Hypothetical SEQUENCE 2

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RESULT 14
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Best Local S
Matches 5
MEDLINE-97443975; PubMed-9298646;
Link A.J., Robison K., Church G.M.;
Link A.J., Robison K., Church G.M.;
Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
-1- FUNCTION: TWO DISTINCT, MEMBRANE-BÖUND, FAD-CONTAINING ENZYMES RESPONSIBLE FOR THE CATALYSIS OF FUMARATE AND SUCCINATE
RESPONSIBLE FOR THE FUMARATE REDUCTASE IS USED IN ANAEROBIC
                                                                                                                                                                                                                                                        Yano M., HOTHUCH. 1.,

*A 718 kb DNA sequence of the E

corresponding to the 12.7-28.0

DNA Res. 3:137-155(1996).
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01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Succinate dehydrogenase iron-sulfur protein (
                                                                                                                       SEQUENCE OF 1-11.
STRAIN=K12 / EMG2;
                                                                                                                                                              SEQUENCE OF 231-238 FROM N.A.
MEDLINE-84236168; PubMed-6376123;
Marlison M.G., Spencer M.E., Guest J.R.;
Darlison et al. Spence of the such gene encoding
"Nucleotide sequence of the such gene encoding
dehydrogenase of Escherichia coli K12.";
Eur. J. Blochem. 141:351-359(1984).
                                                                                                                                                                                                                                                                                                                       Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Oshima T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Itadawa M., Makino K., Masuda S., Mikī T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
STRAIN-K12 / MG16
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Bacteria; Proteobacteria;
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"Nucleotide sequence encoding the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence of Escherichia coli K-12.";
nce 277:1453-1474(1997).
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5; Conserv
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J. 223:507-517(1984).
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EMBL; X01070; CAA25534.1; -.
EMBL; AED00175; AAC73818.1; -.
EMBL; D00711; BAA35391.1; -.
EMBL; X00661; CAA25579.1; -.
PTR; A28837; DEECSI.
SEQUENCE FROM N.,
KO J.H., Lee S.H
"A CDNA encodes
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                                             Dunaliella salina.
Eukaryota; Viridiplantae;
Dunaliellaceae; Dunaliella
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PATHMAY: TRICARBOXYLIC ACID CYCLE.
SUBUNIT: PART OF AN ENZYME COMPLEX
FLAVOPROTEIN, AN IRON-SULFUR, CYTOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF 'PLANT-TYPE' 2FE-2S AND 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS
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COFACTOR: BINDS THREE
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sequence homologous to the eukaryotic
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38;
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fumarate + reduced
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Search completed: August 31, 2002, 12:23:58 Job time: 213 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosomal 5S RNA-binding protein from Dunaliella salina.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIBP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                               EMBL; AF028833; AAB84056.1; -.
InterPro; IPR001149; Ribosomal_L18p.
Iffam; PF00861; Ribosomal_L18p; 1.
PRINTS; PR00058; RIBOSOMALL5.
ProDom; PD001394; Ribosomal_L18p; 1.
Ribosomal protein; rRNA-binding.
SEQUENCE 271 AA; 31218 MW; 482F53833D33B57E CRC64;
                                                                                                 189 DTEVL 193
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## ALIGNMENTS

A;Experimental source: HeLa cells
R;Bonda, H.; Inazawa, J.; Mishida, J.; Yazaki, Y.; Hirai, H.
Blood 84, 4186-4194, 1994
A;Title: Molecular cloning, characterization, and chromosomal localization of a novel
A;Ritle: Molecular cloning, characterization, and chromosomal localization of a novel
A;Reference number: I52599; MUID:95086212
A;Accession: I52599
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecula type: mRNA
A;Residues: I-216,'LTGVRKAA',225-260,'G',262-285,'GTEGGLDASNTERSRA',302,'S',304,'TAPV
A;Cross-references: GB:037781; NID:9633072; PIDN:BAA07035.1; PID:9633073
C;Comment: Enhanced expression of this protein with increasing cell density suggests R;Ostman, A.; Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
A;Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, A;Reference number: I38670; MUID:95024024
A;Accession: I38670 F;1-35/Domain: signal sequence \*\*status predicted <SIG>
F;36-1337/Product: protein tyrosine-phosphatase, receptor type F;36-1337/Product: protein tyrosine-phosphatase, receptor type F;118-197/Domain: fibronectin type III repeat homology <3FNN>
F;206-283/Domain: fibronectin type III repeat homology \*\*status F;284-356/Domain: fibronectin type III repeat homology <3FNN>
F;365-445/Domain: fibronectin type III repeat homology <3FNN>
F;453-530/Domain: fibronectin type III repeat homology <3FNN>
F;593-617/Domain: fibronectin type III repeat homology <3FNS>
F;5720-804/Domain: fibronectin type III repeat homology <3FNS>
F;972-988/Domain: transmembrane \*\*status predicted <TMN> A; Molecule type: mRNA A; Residues: 1-1337 <RES> A; Cross-references: EMBL:U10886; NID:g558754; PID:g558755 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human N;Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphata C;Species: Homo sapiens (man) RESULT I38670 F;1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>
F;72,82,93,104,142,172,192,231,258,278,342,351,376,391,396,413,431,501,525,536,582,60
F;72,82,93,104,142,172,192,231,258,278,342,351,376,391,396,413,431,501,525,536,582,60
F;72,82,93,104,142,172,192,231,258,278,342,351,376,391,396,413,431,501,525,536,582,60
F;72,93,46ctive site: Cys (phosphocysteine intermediate) #status predicted C;Superfamily: protein-tyrosine-phosphatase, receptor type J; i C;Keywords: glycoprotein; phosphorotein; phosphoric monoester A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine C;Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III re C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; t F;1245/Binding C; Function: A;Cross-references: GDB:385040; OMIM:600925 A;Map position: 19q13.4-19q13.4 A; Gene: GDB: PTPRJ C; Genetics: C; Accession: I38670; I52599 C;Date: 01-Mar-1996 #sequence\_revision 08-Mar-1996 #text\_change 22-Jun-1999 site: substrate (phosphocysteine intermediate)
ostrate phosphate (Arg) #status #status predicted predicted atypical <3FNC> ч #status predicted is enhanc ş

Query Match Best Local Similarity

100.0%;

Score 8; Pred. No.

DB 1; 0.19;

Length 1337

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N;Contains: oxidoreductase (EC 1.-.-)
C;Specles: Canis lupus familiaris (dog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: JC4157; S65962; S65898
R;Jiang, Q: Voigt, J.M.; Colby, H.D.
Blochem. Blophys. Res. Commun. 209, 1149-1156, 1995
A;Title: Molecular cloning and sequencing of a guinea pig cytoch.
A;Reference number: JC4153; MUID:95251703
A;Accession: JC4157
                                                                                                                                               R; Jiang, Q.; Voigt, J.M.; Colby, H.D. Biochem. Biophys. Res. Commun. 209, 1149-1A; Title: Molecular cloning and sequencing A; Reference number: JC4153; MUID:95251703 A; Accession: JC4153
                                                                                                                                                                                                                                      cytochrome P450 2D16, CYP2D16 - guinea pig

N;Contains: oxidoreductase (EC 1.-.-.)

C;Species: Cavia porcellus (guinea pig)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000

C;Accession: JC4153; PC4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homolog c;Keywords: adrenal gland; chromoproteln; endoplasmic reticulum; hem F;305-468/Domain: cytochrome P450 homology cP45-F;446/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A; Molecule type: protein
A; Residues: 2-37, 'X', 39 <
C; Comment: This protein i
     0.0
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R;Sakamoto, K:; Kirita, S.; Baba, T.; Nakamura
Arch. Biochem. Biophys. 319, 372-382, 1995
A;Title: A new cytochrome p450 form belonging
A;Reference number: S65898; MUID:95305574
                                       A; Molecule type: protein A; Residues: 1-37 <JI2>
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A;Accession: PC4052
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A; Residues: 1-500 <JIA>
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les 6; Conserv
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                  protein is
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llarity 100.0%;
Conservative
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 ein is a member cytochrome P45(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is a member of the CYP2D subfamily,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <SAW>
                                                                                                                                                                                                    Colby, H.D.
mmun. 209, 1149-1156,
                                                                                            NID: g862481;
     P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6;
Pred. No.
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of the CYP2D subfamily, of the CYP2D6; cytochrome P450
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                                                                                            PIDN: AAA68479.1;
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reticulum; heme;
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                                                                                            PID: 9862482
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     homology
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C;Comment: Residues 1-86 are identical with
C;Superfamily: adenovirus early ElB protein
C;Keywords: early protein
                                                                                                                                                                                                                                  A; Title: Gene organization of the transfo A; Reference number: A91494; MUID:83028529
                                                                                                                                                                                                                                                                                                                      C:Species: Mastadenovirus h7 (human adenovirus A:Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                 WMAD9 early ElB 9K protein I - human adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: adrenal gland; chromoprotein; heme; iron; metalloprotein F;305-468/Domain: cytochrome P450 homology <P45> F;496/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-88 <DIJ>
                                                                                                                                                                                                                                                               Gene 18,
                                                                                                                                                                                                                                                                             R;Dijkema,
                                                                                                                                                                                                                                                                                             C; Accession: A03811
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                                                    Query Match
Best Local S
Matches 5
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44 SRDTE
                          2 SRDTE
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143-156, 1982
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llarity 100.0%;
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A;Cross-references: GB:M85291; NID:g213922 A;Note: sequence extracted from NCBI backbone (NCBIN:88077, NCBIP:88079); this ORF A;Note: the source is designated as Triakis scyllia R:Hashimoto, K.; Nakanishi, T.; Kurosawa, Y. Proc. Natl. Acad. Sci. U.S.A. 89, 2209-2212, 1992 A;Title: Identification of a shark sequence resembling A;Reference number: A41975; MUID:92196087 A;Accession: A41975 major histocompatibility complex class I alpha 3 domain homolog - shark (Tr C;Species: Triakis scyllium C;Date: 26-Aug-1999 #sequence\_revision 26-Aug-1999 #text\_change 26-Aug-1999 A; Molecule type: DNA A; Residues: 1-93 <HAS> A; Status: not compared with conceptual translation C; Accession: Query Match Best Local Matches 1 QSRDT Similarity 5; Conserv A41975 62.5%; nilarity 100.0%; Conservative .08 0; Score 5; Pred. No. Mismatches DB . 51; . د. 0; Length 93; the Indels major shark (Triakis 0; histocompatibility Gaps 0, is

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OSRDT

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N;Alternate names: san protein; single-stranded DNA-binding protein Ssb C:Species: plasmid RK2
C;Date: 18-Feb-1994 #sequence_revision 17-May-1996 #text_change 03-Dec-1999 C;Accession: S07258; A44020; S26289
R;Smith, C.A.; Thomas, C.A.; Thomas, C.A.; Mol. Biol 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S55691

Keratin type I (clone Jn7-4) - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Oct-1995 #sequence_revision 07-Feb-1997 #text_change 10-Dec-1999
C;Accession: S55691
R;Adati, N.; Ito, T.; Koga, C.; Kito, K.; Sakaki, Y.; Shiokawa, K.
Biochim. Biophys. Acta 1262, 43-51, 1995
A;Title: Differential display analysis of gene expression in developing embryos of Xenop A; Reference number: S55691; MUID:95290493
A;Accession: S55691
                                                                                                                                                                                                                                                                                            A;Note: sequence extracted from NCBI backbone (NCBIP:115752)
R;Jagura-Burdzy, G.; Khanim, F.; Smith, C.A.; Thomas, C.M.
Nucleic Acids Res. 20, 3939-3944, 1992
A;Title: Crosstalk between plasmid vegetative replication and conjugative transfer: repr
A;Reference number: S26289; MUID:92375675
                             ρ
                                                                                                                                                                        C;Superfamily: single-stranded DNA-binding protein; C;Keywords: single-stranded DNA binding F;19-95/Domain: single-stranded DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-37 <LES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 267, 20471-20480, 1992
A;Title: Sequence similarities between the RP4 Tra2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X00713; NID:g45775; PIDN:CAA25305.1; PID:g45776 A;Note: the authors translated the codon CAC for residue 64 as Gln R;Lessl, M.; Balzer, D.; Pansegrau, W.; Lanka, E. J. Biol. Chem. 267, 20471-20480, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Smith, C.A.; Thomas, C.M.
J. Mol. Biol. 175, 251-262, 1984
A;Title: Nucleotide sequence of the trfA gene
A;Reference number: S07258; MUID:84216332
A;Accession: S07258
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                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                             A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A44020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A44020; A; Contents: incompatibility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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A; Residues: 1-105 <ADA>
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R; Johnson, G.F.
submitted to GenBank, June
submitted to momber: A33172
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A; Accession: H24481
A; Molecule type: DNA
A; Residues: 1-129 < ROS>
A; Cross-references: GB:M13209; NID:g335739;
C; Superfamily: vaccinia virus H8 protein
C; Keywords: late protein
A;Cross-references: GB:M35027; NID:g335317; C;Superfamily: vaccinia virus H8 protein C;Keywords: late protein
                                                                                                                                                                        H8 protein - vaccinia virus (strain N;Alternate names: H7R protein C;Species: vaccinia virus C;Date: 30-Sep-1992 #sequence_revisi C;Accession: G42514
                                                        A; Reference number: A33:
A; Accession: G42514
A; Molecule type: DNA
A; Residues: 1-146 < JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Rosel, J.L.; Earl, P.L.; Weir, J.P.; Moss, J. Virol. 60, 436-449, 1986
A;Title: Conserved TAAATG sequence at the tr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: H24481
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A;Experimental source: specific host Chlorella strain NC64
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A; Residues: 1-118 <GRA>
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A;Accession: T17967
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERV1 protein homolog A465R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             2 SRDTE 6
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100.0%; Pr
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62;
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67;
                                        PIDN:AAA48094.1; PID:g335442
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probable 17K protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A:Variety: Strain Ankara
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T37373
R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain A:Reference number: Z20877
A:Accession: T37373
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 1-146 <ANTY
A:Cross-references: EMBL:U94848; PIDN:AAB96510.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA097R
C:Superfamily: vaccinia virus H8 protein
                                                                                                                                                                                                                                                                                                                                          dynein heavy chain 3 - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jui-2000
C;Accession: $72241
R;Porter, M.E.; Knott, J.A.; Myster, S.H.; Farlow, S.J.
Genetics 144, 569-585, 1996
A;Title: The dynein gene family in Chlamydomonas reinhardtii.
A;Reference number: $72239; MUID:97044450
A;Accession: $72241
A;Accession: $72241
A;Status: preliminary; nucleic acid sequence not shown
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S72241
                 hypothetical protein all3520 [imported] - C; Species: Anabaena sp.
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AI2245
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A; Introns:
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A; Residues: 1-147 < POR>
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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Pred. No. 74;
0; Mismatches
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Pred. No.
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Pred. No.
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GB:AP001519;

GB:BA000004; NID:g10176109; PIDN:BAB07305.1;

GSPDB:G

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C;Species: Caudina arenicola
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 19-May-2000
C;Accession: S15979
R;Mauri, F; Omnaas, J; Davidson, L; Whitfill, C; Kitto, G.B.
Blochim. Biophys. Acta 1078, 63-67, 1991
A;Title: Amino acid sequence of a globin from the sea cucumber Caudina (MolF A;Reference number: S15979; MUID:91265540
A;Accession: S15979
A;Molecule type: protein
A;Residues: 1-158 <BIO>
                                                                                                                                                                                                                                                                                     acetyltransferase BH3586 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (c;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: BH098 R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N.; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: globin; globin homology C;Keywords: blocked amino end; blood; chromoprotein; dimer; erythrocyte; heme; iron; F;12-157/Domain: globin homology <GLB>
F;11/Modified site: blocked amino end (Gly) (probably acetylated) #status experimental F;73/Binding site: oxygen (His) (distal axial ligand) #status predicted F;704/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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A;Accession: AI2245
A;Accession: AI2245
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A; Molecule type: DNA
A; Residues: 1-166 <S
A; Cross-references:
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A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: al13520
                                                                                                                                            A;Reference number: A83650;
A;Accession: B84098
                                                                                                                                                                              R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
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A; Residues: 1-154 <KUR>
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; Yasuda, M.; Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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		Search completed: August 31, 2002, 12:20:42 Job time: 122 sec	Query Match 62.5%; Score 5; DB 2; Length 166; Best Local Similarity 100.0%; Pred. No. 83; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Experimental source: strain C-125 C;Genetics: A;Gene: BH3586

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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
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Match Length DB
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747574 seqs, 111073796 residues
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Copyright (c) 1993 - 2000 Compugen Ltd
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                             AAU03200
AAR85203
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AAX66911
AAR51956
AAB03844
AAB03844
AAB05149
AAG09826
AAU54869
                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                          Sequence #1 for ep hubEP-1. Homo sap Drosophila melanog T cell antigen rec Lipopolysaccharide Peptide Q0130 used Peptide Dof peptide Maize Dof peptide ERA binding domain
                                                                                                                                                                                                                                                                                                     Description
Propionibacterium Human protein SEQ
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Novel human diagno	ABG08331	22	293	:-	U	45
rosophila mela	ABB64520	22	290	:-	ı Uī	4.4
S. epidermidis ope	AAG82613	22	287	:-	U	43
dopsis	AAG54774	21	286	:~	U	4.2
	AAU01781	22	284	:~	ı G	41
	AAG32239	21	280	:~	G	40
	AAG32240	21	271		ı G	9
Human inflammation	AAY94451	21	265	62.5	ı UI	0
വ	ABB69076	22	250	.~	G	37
Human olfactory re	AAG72257	22	246	.~	U	36
pylori ORF 11a	AAW55386	18	227	.~	υī	. ω . σ
lori G	AAW98427	19	223	.~	G	34
Amino acid sequenc	AAY37759	20	222	.~	U	i G
ebacterium q	AAB80153	22	219	.~	U	32
el human secre	AAU30554	22	216	~	տ	31
lori ORF 2	AAW55524	18	200	~	٠ G	30
Human N-acetyl tra	AAY69981	21	178	$\sim$	ı G	29
⋖	AAB25184	21	151	.~	U	28
	ABG16051	22	147	~	U	27
	AAB57124	21	131	N	υī	26
human dia	ABG18304	22	127	N	U	25
Human secreted pro	AAG01891	21	121	N	ı Uı	24
Propionibacterium	AAU53773	22	118	N		23
Propionibacterium	AAU39232	22	118	2	G	22
	AAY50927	21	116	N	U	21
Q.	AAM36511	22	105	N	U	20
bone marrow	AAM76402	22	105	N	տ	19
Human brain expres	AAM63587	22	105	N	رب ر	18
Propionibacterium	AAU67333	22	93	N	ر.	17
bacterium	AAU63362	22	93	Ν	ر ت	16
in fragment	AAB03842	21	90	2	G	15
ein fragment	AAB03841	21	90	2	υ	14
	AAR25119	¥ 3	72	Ν	տ	13
Human polynentide	AAM39020	22	68	Ν	տ	12

## ALIGNMENTS

RESULT

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PT mig:
PT pho: Novel antibody for modulating angiogenesis and endothelial cell migration and proliferation, binds endothelial cell receptor tyrosine phosphatase/density enhanced phosphatase-1 WPI; 2001-570681/64. ECRTP/DEP-1; endothelial cell receptor tyrosine phosphatase; density enhanced phosphatase-1; anti-inflammatory; antipsoriatic; antiheumatic; antidiabetic; antiatherosclerotic; cytostatic; osteopathic; angiogenesis inhibitor; tumour; cancer. 01-MAR-2000; 2000US-0516728 27-FEB-2001; 2001WO-US06178 07-SEP-2001. Mammalia. (UYVA-) UNIV VANDERBILT. WO200164750-A2 Sequence #1 for epitope of ECRTP/DEP-1 ectodomain binding antibody. 03-JAN-2002 AAU03200; AAU03200 standard; peptide; 8 то, Takahashi T, (first entry) Mernaugh À

Example 4; Page 82;

110pp; English

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a novel purified antibody (or its fragment or derivative) which preferentially binds an endothelial cell receptor tyrosine phosphatase/density enhanced phosphatase-1 (ECREP/DEP-1). The antibody has antiinflammatory, antipsoriatic, antirheumatic, antidiabetic, antiatherosclerotic, cytostatic and osteopathic activities antidiabetic, antiatherosclerotic, cytostatic and osteopathic activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          such as solid tumours, solid tumour metastases, angiofibromas, retrolental fibroplasia, hemangiomas, Kaposi's sarcoma and similar cancers. This sequence is peptide sequence #1 for epitope ECRTP/DEP-1 ectodomain binding antibody used to modulate angiogenesis, described the method of the invention.

Note: This sequence for ECRTP/DEP-1 epitope, given in example 4, different that given in claim 3 (AAU08802).
                                                                                                                                                                                                                                                                                                                      09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                   WO9530008-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  huDEP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
A cDNA clone was obtd. (see AAT06027) from
                                       Claim 4; Page 34-38; 51pp; English
                                                                                                                                     WPI; 1995-393079/50.
N-PSDB; AAT06027.
                                                                                                                                                                                      Oestman A,
                                                                                                                                                                                                                                                       03-MAY-1994;
                                                                                                                                                                                                                                                                                       03-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 Density enhanced
                                                                                     New density enhanced protein tyrosine phosphatase - used to develop prods. to modify transcription, translation and/or activity of
                                                                                                                                                                                                                                                                                                                                                                                                                    huDEP-1.
                                                                     tyrosine phosphatase(s).
                                                                                                                                                                                                                     (COLD-) COLD SPRING HARBOR LAB
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Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that encoded a novel density-enhanced Type III receptor-like PTP, designated huDEP-1 (AAR85203). huDEP-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for prevention of abnormal or malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling (cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ
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                                                                                                                                                                            Disclosure; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                    The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                New isolated nucleic a
genes from Drosophila
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                       at ftp.wipo.int/pub/published_pct_sequences
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                                                              ABB57737-ABB72072)
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DB; ABL05141.
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2000US-0614150.
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                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to peptide sequences present in the synovial fluid and membranes of rheumatoid arthritis patients, arising from the CDR region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains. Compositions which contain autoantigenic peptides binding specifically to T-cells expressing receptors containing the peptide sequences, which include antigen-specific immunological tolerance to rheumatoid arthritis can be used for the treatment and prevention of rheumatoid arthritis. The invention can be used for the diagnosis, treatment and prevention of rheumatoid arthritis. Sequences AAY66771-958 represent peptides from the various Vbeta chains of T cell antigen receptor.
     Lipopolysaccharide induced
                                                            24-MAY-1994
                                                                                                                AAR51956;
                                                                                                                                                               AAR51956 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 103; 136pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishioka K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1998;
14-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09963084-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T cell antigen receptor Vbeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY66911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vbeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450
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| qsrdte 455
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98JP-0328761.
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protein (peptide fragment).
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Matches 5
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                                                                                                                                                                                                                                                                                                     Serum type identify; t
                                                    29-OCT-1998;
                                                                                                    29-OCT-1998;
                                                                                                                                                      16-MAY-2000
                                                                                                                                                                                                        JP2000135087-A
                                                                                                                                                                                                                                                                                                                                  Serum
                                                                                                                                                                                                                                                                                                                                                                            Peptide Q0130 used in TT virus antibody determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB03843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB03843 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 67; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide induced in macrophage(s) by useful e.g. as antitumour, antiinflammatory agent, also related nucleic acid, antibodies
                                                                                                                                                                                                                                                        TT virus
                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000
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treatment.
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                                                                                                                                                                                                                                                                                                                          TT virus; antibody; viral infection;
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3. 26;
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Best Local
                                                                                                                        A method for serum type classification of TT virus (also known as hepatitis TT virus) has been identified. The method relies on the use of peptide fragments of the virus. The invention also relates to the use of TT virus peptides for anti-TT virus antibody determination. The anti-TT virus antibodies and the serum type classification method, can be used to screen TT virus, to determine its route of infection, and seroconversion. The classification of TT virus may lead to improved treatment of viral disease. The present sequence represents a fragment of TT virus protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method for serum type classification of TT virus (also known as hepatitis TT virus) has been identified. The method relies on the use of peptide fragments of the virus. The invention also relates to the use of TT virus peptides for anti-TT virus antibody determination. The anti-TT virus antibodies and the serum type classification method, can be used to screen TT virus, to determine its route of infection, and seroconversion. The classification of TT virus may lead to improved treatment of viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides for determination of anti-TT virus antibody and method serum classification of TT virus using the peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide R0130 used in TT virus antibody determination
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                                                                                             used
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                                        The invention relates to a transgenic monocot plant comprising an isolated DNA operably linked to a promoter, which is expressed to yield a prolamin box binding factor peptide (PBF). PBF then binds to promoter regions of 22-kD alpha-zein (prolamin seed storage proteins of promoter regions of 22-kD alpha-zein (prolamin seed storage proteins of maize are named zein) and 27-kD gamma-zein genes, so as to enhance gamma-zein production and lower alpha-zein production, so that methionine and lysine content of plant seed is increased over the content in native plant. PBF protein is a novel endosperm-specific cys2-cys2 zinc finger-type DNA binding protein of the DDF family. The transgenic monocot plant is a maize plant and expresses increased levels of methionine and/or lysine content in the seeds of the plant. The development of transgenic lines which supply higher levels of methionine reduces the need for methionine supplements for corn-soybean meal poultry feed and conceased lysine content of either the cereal grains or the oilseed crops results in significant added nutritional value. The present is maize of methionine domain ZMDOF2. This sequence contains a dof domain at the
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nutritional value; ZMDOF2
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AAM78696
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Conservative

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Mismatches

Indels

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RESULT

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AAM78696

standard;

Protein;

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Best Loc
Matches
                                    Query Match
                                                                                                                                         presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central process is also involved in infections of bone, joints and the central process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucleic acids useful vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-2000;
02-JUN-2000;
                                                                                         Sequence
                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID No 16064; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPHO syndrome; synovitis; acne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein #15765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-FEB-2002
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                   Local
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DB; AAS59566.
Similarity
5; Conser
                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
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e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                         AA;
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                 62.5%;
100.0%;
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, Jen S, Carter D;
                   Score 5;
Pred. No.
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                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypertosis; osteomyelitis;
                                    Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bhatia A;
                                                                                                                                               part of the printed directly from WIPO
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are used in
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RESULT 1
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Best Local Similarity
                                                                                                                                                                                                                                                            The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis regulating activity, thissue growth factor activity. The diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang
Zhao
           AAM39020 standard;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                             Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                           useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAK51829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-2000;
20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-2000;
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                                                                                                                                                                                                                                                    inflammation.
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                                                                                      1 QSRDT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein SEQ ID NO 1358
                                                                                                                                                                                                                                                                                                                                                                                                    20; Page 3607; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
Wang D,
Yang Y,
                                                                                                                                                                                        89
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2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-06633251.
2000US-0693325.
2000US-0728422.
                                                                                                                            Conservative
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Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
           Protein;
                                                                                                                                     62.5%;
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                                                                                                                         Score 5; DB 2; Pred. No. 91; 0; Mismatches
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                                                                                                                                                  Length 68
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                                                                                                                                                                                                                         (AAK52582) and 3666 the sequence listing
                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          activities
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Local Similarity nes 5; Conserv

62.5%; ilarity 100.0%; Conservative

Score 5; pred. No 0,

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21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0652036.

19-CGT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, cancer diagnosis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; halzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
Sequence
                                                                                            C.N.S disorders
                                              specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM39020;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO 2165; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
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DB; AAI58176.
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Zhou P,
                                                                      sequence
  68
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  AA;
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Wehrman T, X
Goodrich R,
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                                                                         data
                                                                         for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides, useful
system injuries -
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Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac F
                                                                      patent did not
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e AJ,
RT;
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Zhang J;
                                                                         of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
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Best Local
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29-NOV-1990;
16-JAN-1991;
19-APR-1991;
07-JUN-1991;
                                                                                                                                                                                                                                        This sequence is one of 12 claimed antigen sequences specific to NANBH virus. The antigens can be used singly or in combination in an ELISA diagnosis of hepatitis. See AAR24946 and AAR25110-R25121
        16-MAY-2000
                      JP2000135087-A.
                                     TT virus
                                                   identify;
                                                          Serum type classification;
                                                                       Protein fragment #3 used in TT virus antibody determination
                                                                                       20-OCT-2000
                                                                                                      AAB03841;
                                                                                                                    AAB03841 standard; protein;
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                     Claim 1; Page 49;
                                                                                                                                                                                                                                                                                    specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen
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                                                                                                                                                                                             Local
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pific detection of hepatitis
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                                                    treatment.
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                                                                                       (first
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90JP-0325435.
91JP-0070231.
91JP-0179074.
91JP-0232590.
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                                                                                                                                                                                                                                                                    80pp; Japanese.
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                                                                                                                                                                                   62.5%; 5c,
100.0%; Pr
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                                                                                                                                                                                             Score 5; Pred. No.
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                                                          virus;
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                                                          antibody;
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                                                                                                                                                                                          DB
96;
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                                                          viral infection,
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                                                                                                                                                                                                                                                                                    Serum type classification;
                                                                                          Peptides for determination of anti-TT virus antibody serum classification of TT virus using the peptides
                                                                                                                                                                     29-OCT-1998;
                                                                                                                                                                                          29-OCT-1998;
                                                                                                                                                                                                              16-MAY-2000
                                                                                                                                                                                                                                  JP2000135087-A
                                                                                                                                                                                                                                                        TT virus
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                                                                                                                                                                                                                                                                                                                                20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                     AAB03842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides for determination of anti-TT virus antibody serum classification of TT virus using the peptides
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                                                                                                                                                (SRLS-) SRL KK
                                                                                                                                                                                                                                                                            identify;
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                                                                                                                                                                                                                                                                             treatment
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                                                                                                                                                                                                                                                                                       viral infection;
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A method for serum type classification of TT virus (also known as hepatitis TT virus) has been identified. The method relies on the use of peptide fragments of the virus. The invention also relates to the use of TT virus peptides for anti-TT virus antibody determination. The anti-TT virus antibodies and the serum type classification method, can be used to screen TT virus, to determine its route of infection, and seroconversion.

, can be used to seroconversion.

Claim 3; Page

8; 12pp; Japanese

SSSSS

Sequence 90 AA;

The classification of TT virus may lead to improved treatment of viral disease. The present sequence represents a fragment of TT virus protein used in the course of the invention.

Search completed: August 31, 2002, 12:20:01 Job time: 231 sec

Вb δÃ

3 RDTEV 7 ||||| 26 rdtev 30

Query Match 62.5%; Score 5; DB 21; Le Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0;

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Q9npr5 homo sapien Q15255 homo sapien Q15255 homo sapien Q90h7 mus musculu Q9ky21 streptomyce Q93gk2 klebsiella Q9c923 arabidopsis Q9jgs8 tt virus. p Q9jgs5 tt virus. p Q9jgs2 tt virus. p Q9jgs2 tt virus. p Q9ys21 mus musculu Q9w4m7 drosophila Q9wux1 rattus norv Q917u3 tt virus. o Q917u3 tt virus. o Q22031 cyanidium c Q91404 xenopus lae
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## ALIGNMENTS

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1 OSRDTEVL 8          324 QSRDTEVL 331	Query Match 100.0%; Score 8; DB 4; Length 425; Best Local Similarity 100.0%; Pred. No. 0.12; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	NON_TER 425 425 SEQUENCE 425 AA; 45078 MW; BD1ACA5D345B7027 CRC64;	SMART; SM00060; FN3; 2.	InterPro; IPR003961; FN_III.	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; $\Delta L359057$ ; $CAB94390.1$ ;	human gene transcripts.";	A., Lundeberg J.;	SEQUENCE FROM N.A. Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,		Andreu N., Estivill X., Escarceller M., Sumoy L.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.		NCBI_TaxID=9606;	Catarrhini; Hominidae;	Fishervote: Moteraros: Chordate: Crantate: Vottobrate: Fisheloogtomi:	PTPRJ, PROTEIN TYROSINE PHOSPHATASE RECEPTOR J, ETA (FRAGMENT).	(TrEMBLrel. 17, Last annotation update)	01-007-2000 (TrEMBErel. 15, Created)		Q9NPR5 PRELIMINARY; PRT; 425 AA.	RESULT 1

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RESULT

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InterPro; IPR003961; FN_III
InterPro; IPR003961; FN_III
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InterPro; IPR000242; Tyr_prot_phphtase.
InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00041; fn3; 5.
Pfam; PF00102; Y_phosphatase; 1.
PFINTS; PR00700; PRTYPHPHTASE.
SMART; SM00060; FN3; 6.
SMART; SM00060; FN3; 6.
SMART; SM000194; PTPC; 1.
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Q15255;
Q1-NOV-1996
Q1-NOV-1996
   STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=2108560; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.
                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2610016F07RIK PROTEIN.
POV1 OR 2610016F07RIK.
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HSSP;
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SIGNAL
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PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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D37781; BAA07035.1; -.
P18052; 1YFO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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**A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome.

**Mol. Microbiol. 21:77-96(1996).

**EMBL; AL356892; CAB92845.1; -

**SEQUENCE 152 AA; 16984 MW; 4A315E60E7D853AO CR
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Bentley S.D., Parkhill J
Submitted (MAY-2000) to
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Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Streptomyces coelicolor.
Bacteria; Firmicutes; Ac
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PUTATIVE THIOL-SPECIFIC
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EMBL; AK011417; BAB27605.1; -.
MGD; MGI:1931352; Pov1.
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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Hujia C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
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F14G24.25.
                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"Structure, organization and characteri
involved in the production of microcin
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EMBL; AF063590; AAL08403.1; -.
SEQUENCE 524 AA; 59120 MW; 2F
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MEDLINE=21537172; PubMed=11679081;
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                     Q9JGS8;
01-OCT-2000
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         Viruses; ssDNA vi
NCBI_TaxID=68887;
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                           TT virus.
                                                                                Q9JGS5
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EMBL; AB030487; EAA90406.1; -
InterPro; IPR004219; TT_ORF1.
Pfam; PF02956; TT_ORF1; 1.
SEQUENCE 765 AA; 90225 MW; E8
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NCBI_TaxID=68887;
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InterPro; IPR002917; MMR_HSR1.
Pfam; Pf01926; MMR_HSR1; 1.
PRINTS; PR00326; GTP10BG.
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EMBL; AC019018; AAG52287.1;
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MEDLINE=20417334; PubMed=10963344;
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090XG1; 01-MAY-2000 (TrEMBLrel. 13,
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Mammalia; Eutheria;
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MEDLINE-20417334; Pubmed-10963344;

Tanaka Y., Orito E., Ohno T., Nakan,

Mukaide M., Iida S., Mizokami M.;

"Identification of a 23kDa protein
frame 2 of TT virus (TTV) genotype
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genotypes.";
%rch Virol. 145:1385-1398(2000).
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Arch. Virol. 145:1385-1398(2000).
         Bartman A.E.,
                                    SEQUENCE FROM
                                                                                                                                                                                    Mus musculus (Mouse).
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Mukaide M., IIda S., Mizokami M.;
"Identification of a 23kDa protein
frame 2 of TT virus (TTV) genotype
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MEDLINE=20417334; PubMed=10963344;
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Pro; IPR004219; TT_ORF1.
PF02956; TT_ORF1; 1.
NCE 765 AA; 90401 MW;
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Pro; IPR004219; TT_ORF1.
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b; Pred. No. 38;
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Sciurognathi;
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         R.E.,
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RX MEDLINE-20199006; Pubmed=10/31132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Boxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Boxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.G., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., I.J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., I.J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
                                  ACOCCA PROBLEM RADING R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멍
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SMART; SM00181; EGF_like; 2.
SMART; SM00001; EGF_like; 2.
SMART; SM00539; NIDO; 1.
SMART; SM00216; VWD; 1.
SMART; SM00216; VWD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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Q9W4M7: 097423; 097424;
01-MAY-2000 (TIEMBLICEL II:
01-MAY-2000 (TIEMBLICEL II:
01-OCT-2001 (TIEMBLICEL II:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Ho
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG4857 OR EG: EG0007.4 OR
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EMBL; AF218265; AAF2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ho S.B.;
"Identification and Structure of a Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
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InterPro; IPR003886; Nidogen_ext.
InterPro; IPR001846; Vwd.
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5. 62;
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O9WUX1;
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O1-NOV-1999 (TrEMBLrel. 12, Cre
O1-NOV-1999 (TrEMBLrel. 12, La:
O1-NOV-1999 (TrEMBLrel. 12, La:
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Science 287:2220-2222(2000).
EMBL; AE003430; AAF45924.1; -
EMBL; AL033125; CAA21827.1; AIT_SEQ.
EMBL; AL033125; CAA21828.1; AIT_SEQ.
ENBL; AL033125; CAA21828.1; AIT_SEQ.
E1yBase; FBqn0026083; CG4857.
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Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadie
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Bork
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov s
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.G.
Glover D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., 
                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=98335789; Greeve J., Axelos
                                                                                                                                                                                      Arterioscler.
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Hypothetical
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  Similarity 5; Conserv
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D., Welker S.,
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                     Score 5; |
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  Mismatches
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Q1-DEC-2001
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NON_TER
SEQUENCE
                                                                                                                      Yu J.G., Shang Q.H., Ren H.;
"Transfusion transmitted vir
Submitted (SEP-2001) to the
EMBL; AF416142; AAL15658.1;
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                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2001) to the EMBL; AF416141; AAL15657.1; NON_TER 1
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NCBI_TaxID=68887;
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virus (TTV)
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Search completed: August 31, 2002, 12:23:05 Job time: 215 sec
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                                                                                                                                                                                                Ohta N.;

Ohta N.;

J. Plant Res. 110:235-245(1997).

EMBL; D63676; BAA22827.1; -.

HSSP; P00274; 1T7P.

InterPro; IPR000063; Thiored.
Pfam; PF00085; thiored; 1.

PRINTS; PR00421; THIOREDOXIN.
PROSITE; PS00194; THIOREDOXIN; 1.

Redox-active center.

Redox-active center.

SEQUENCE 101 AA; 11476 MW; 7678E87CFB82B098 CRC64;
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O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
THIOREDOXIN M.
TRXM.
Cyanidium caldarium.
Cyanidium.
Charyota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
Cyanidium.
NCBL_TaxID-2771;
[1]
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STRAIN=RK-1;
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9 DTEVL 13
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Maximum Match 100%
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3: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1981.DAT: *
4: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1982.DAT: *
4: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1982.DAT: *
5: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1984.DAT: *
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7: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1985.DAT: *
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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AAG1481113
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29.620 Million cell updates/sec
             Sequence #1 for ephubEp-1. Homo sap Human secreted pio Arabidopsis thalia                                                                                                                                                                                                                                                                                                  Description
Human transcriptio
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7	7	28 7	28 7	28 7	28 7	28 7	28 7	7	28 7	28 7	28 7	28 7	2 28 7	1 28 7	0 28 7	9 28 7	28 7	7 29 7	29 7	29 7	29 7	29 7	29 7	29 7	30 7	30 7	30 7	30 7	30 7	30	30 7	13 30 7	30
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phthalene di	മ			1 human			olypep	#301	#320	Peptide #310 encod	bone m	rain e	#302	e #327	Human peptide #302	Protein encoded by	Swinepox virus Hin	Drosophila melanog			epto	CFE 100 protein se	Drosophila melanog	Streptococcus pneu	Ö					an pol	mays protein	mays prote	protein

## ALIGNMENTS

Sequence #1 for epitope of ECRTP/DEP-1 ectodomain binding antibody.

03-JAN-2002 AAU03200;

(first entry)

AAU03200 RESULT

ب

AAU03200 standard; peptide;

8 A

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Novel antibody for modulating angiogenesis and endothelial cell migration and proliferation, binds endothelial cell receptor tyrosine phosphatase/density enhanced phosphatase-1 -
                                                                                                                                                                                                                                                  ECRTF/DEP-1; endothelial cell receptor tyrosine phosphatase; density enhanced phosphatase-1; anti-inflammatory; antipsoriatic; antirheumatic; antidiabetic; antiatherosclerotic; cytostatic;
                                                 WPI; 2001-570681/64.
                                                                                                                    01-MAR-2000; 2000US-0516728
                                                                                                                                                                   07-SEP-2001
                                                                                                                                                                                                                                       osteopathic;
                                                                        Daniel TO,
                                                                                              (UYVA-) UNIV VANDERBILT.
                                                                                                                                            27-FEB-2001; 2001WO-US06178
                                                                                                                                                                                           WO200164750-A2
                                                                                                                                                                                                                  Mammalia.
                                                                      Takahashi T,
                                                                                                                                                                                                                                       angiogenesis inhibitor; tumour; cancer.
                                                                      Mernaugh R;
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RESULT
AAR85203
ID AAR8
XX AAR8
XX AAR8
XX AAR8
XX DAR8
XX DENS
KW DENS
KW DO95
XX WO95
XX WO95
PM O9-1
XX O9-1
XX OP-1
XX OP-
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Note: This sequence for ECRTP/DEP-1 epitope, given in example 4, differs from that given in claim 3 (AAU08802).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine phosphatase/density enhanced phosphatase-1 (ECRTP/DEP-1). The antibody has antiinflammatory, antipsoriatic, antirheumatic, antidiabetic, antiinflammatory, antipsoriatic, and osteopathic activities and may be an ECRTP/DEP-1 modulator, ECRTP/DEP-1 dimerisation promoter or antagonist and angiogenesis inhibitor. The purified antibody blocks endothelial migration and proliferation and inhibits angiogenesis in disorders such as inflammatory disorders including immune and non-immune inflammation, chronic articular rheumatism and psoriasis, disorders associated with inappropriate invasion of vessels such as diabetic
A cDNA clone was obtd.
                                                                     Claim 4; Page 34-38; 51pp; English
                                                                                                                                                                            New density enhanced protein tyrosine phosphatase - used to develop prods. to modify transcription, translation and/or activity of
                                                                                                                                                                                                                                                                                      N-PSDB; AAT06027
                                                                                                                                                                                                                                                                                                                          WPI; 1995-393079/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COLD-) COLD SPRING HARBOR LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Density enhanced
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                                                                                                                                           phosphatase(s).
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                                                                                                                                                                                                                                                                                                                                                                                                    Tonks NK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9405-0237940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US05512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Туре
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             III receptor-like protein tyrosine phosphatase,
       (see AAT06027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DE Pred. No. 6.4
); Mismatches
       from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
       ø
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       HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
       cell cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local Similarity
"hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG01891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                               The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs with intact 5' under the sequences derived from mRNAs under the sequences derived from mRNAs under the sequences derived from mRNAs un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45.
N-PSDB; AAC01897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that encoded a novel density-enhanced Type III receptor-like PTP, designated hubEp-1 (AAR85203). hubEp-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for prevention of abnormal or malignant cell growth.
Sequence
                                                                                                                                                                                                                                                                                                                                                                    Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG01891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG01891 standard; Protein; 121
                                                                                                              ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033401-A2
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                                                                    chromosome
                                                                                       DNAs. 5' ESTs are also used in diagnostic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST;
                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 5972;
                                          sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1337 AA;
  121
                                                                                                                                                                                                                                                                                                                                                                                                              forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome mapping.
  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed sequence tag; secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein, SEQ ID NO:
                                                               procedures. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                               and to
                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy and
                                                                                                                                                                                                                                                                                                                                                                 71pp + CD-ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duclert A,
                                               design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5972.
                                               expression
                                                                  nostic, forensic, gene therapy and are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Giordano J;
                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                               and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1337;
                                                                                                                                                                                                                                                                                                                                                                                                              mapping procedures
                                               secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Query Match Best Local S Matches 6

Similarity 6; Conser

Conservative

81. 75.

. 6%;

Score 31; DB Pred. No. 55; 1; Mismatches

21;

Length 121;

Indels

0;

Gaps

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FEB-1999
MAR-1999
MAR-1999
APR-1999
APR
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| qsrdtpil 120
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990S-0125788.
990S-0126785.
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990S-0129845.
990S-0130449.
990S-0131484.
990S-0131486.
990S-0132487.
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expression control;
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promoter;
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  14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
                                   New isolated nucleic a
genes from Drosophila
interactions -
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N-PSDB; ABL08914.
 Disclosure; SEQ ID NO 21225; 21pp + Sequence Listing; English
   (PEKE
  23-MAR-2000;
11-JUL-2000;
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   Venter JC,
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  Drosophila melanogaster
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2000US-0614150
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  249
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   990S-0159294.
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990S-0161393.
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75.0%;
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   543
   Myers
   ΑA
   SEQ
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   Db __
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                          The present sequence is the protein sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative, autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification,
  Hillman
Azimzai
  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
   Novel transcription factor polypeptides, used to treat diseases associated with altered activity and expression of TRFX, and to for agents capable of modulating its activity -
   04-OCT-2001
allergies,
               including:
  Claim
   N-PSDB;
  13-MAR-2000; 2000US-0188986
  neuroprotective; antiinflammatory; gene therapy.
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developmental
  Human transcription
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   ABB50168;
  Sequence
   at ftp.wipo.int/pub/published_pct_sequences
  The sequence data for this patent did not form specification, but was obtained in electronic i
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DB; ABA82992.
  sapiens.
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arteriosclerosis,
anaemia, asthma, a
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05-MAR 1999

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14-MAY 1999

15-MAY 1999

19-MAY 1999

20-MAY 1999

21-MAY 1999
  dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's disease, stroke, and viral, bacterial, fungal and protozoal infections.
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| אַר                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | אס<br>אס<br>אס<br>אס<br>אס<br>אס<br>אס<br>אס<br>אס<br>אס           |
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The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM4347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
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Conservative

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Score 38; DB Pred. No. 3; Mismatches

DB ω 0;

Length 1337; Indels

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30 31	4 223 1 US-07 4 223 1 US-07 4 223 1 US-07 4 223 1 US-07	Sequence 3, Ap Sequence 3, Ap Sequence 3, Ap
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ယ ယ တ <b>ဟ</b>	6 68.4 447 2 US-08-902-585-2 6 68.4 650 1 US-08-121-713D-	
37 8	6 68.4 650 1 US-08-835-268-6	Sequence 60,
. ພ ເ	6 68.4 650 3 US-08-833-391-6	Sequence 60,
410	6 68.4 650 5 PCT-U	Sequence 60,
4 4 2	6 68.4 1462 3 US-07	Sequence 31,
4.4.	6 68.4 1462 3 US-09 6 68.4 1745 2 US-09	Sequence 31, Appl
	ALIGNMENTS	
RESULT 1 JS-08-854- ; Sequence	285	
GENERAL APPLIC	INFORMATION: ANT: Tonks, Nicholas K	ne
NUMBER	NUMBER OF SEQUENCES: 6  CORRESPONDENCE ADDRESS:	
AD ST	Marshall, O'Toole, Gerstein South Wacker Drive, Suite	6300 & Borun
COL	TRY	
COMPUT	60606 ER READABLE FORM:	
0 3	IBM PC compatible	
CURR	OPERALING SISTEM: PURCHASE #1.0, Version SOFTWARE: PatentIn Release #1.0, Version URRENT APPLICATION DATA:	1 #1.25
AP FI	APPLICATION NUMBER: US/08/854,585 FILING DATE:	
AP	APPLICATION NUMBER: US/08/237,940 FILING DATE:	
ATTO	AGENT INFORMATI	
RE	BER: 25,447	
TELE	ELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300	
TELEFAX	: 312-474-0448	
SEQU	HARACTERISTICS:	
YI.	amino acid	
MOLE	ΞG	

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; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-387-695-2
                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: May, Earl
APPLICANT: Van Horn, Stephanie
APPLICANT: Warren, Patrick V.
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: dome
                                                                                                                                                                                                                                                                                                                                                                     US-09-387-695-2

; Sequence 2, Application US/09387695

; Patent No. 6280990
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PCT-US95-05512-2
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                                                                                                              SEQ ID NO 2
LENGTH: 1042
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GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
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Best Local Similarity
Matches 8; Conserv
Query Match
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ZIP: 60606
ZIP: 60806
COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
MEDDIUM TYPE: IBM PC compatible
TWOTTER: IBM PC-DOS/MS-DOS
TWOTTER: PC-DOS/MS-DOS
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/387,695 CURRENT FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
                                                                                                                                                       SOFTWARE: FastSEQ
                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                 FILE REFERENCE: GM10237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447 REFERENCE/DOCKET NUMBER: 27/ TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Borun, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 QSRDTEVL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                     for Windows Version 3.0
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76.3%;
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Score 29;
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DB 4;

Length 1042;

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US-09-172-977-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/172,977
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1336 RSRDVEVL 1343
                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                        STATE: I
                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                          CITY: Gainesville
                                                                                                                                                                                                                                                                                                          STREET:
APPLICATION NUMBER:
                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                    Florida
Y: U.S.A.
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.3%;
75.0%;
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                                                 US 07/908,241
US 07/908,630
                                                                                                                   US/08/307,499
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4.2e+02;
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PRIOR APPLICATION DATA:

US 07/342,212

FILING DATE: 29 CLASSIFICATION:

29-JUN-1992

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-299-268-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09299268 Patent No. 6217882
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus
TITLE OF INVENTION: Live Vaccine Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UTELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
TELEPHONE: 904-372-5800
TELEPHONE: POP CEO TO TO TELEPHONE: POP CEO TO TELEPHONE: POP CEO TO TO TELEPHONE: POP CEO TO TO TO TELEPHONE: STATE TO TO TELEPHONE: STATE TO TELEPH
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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NAME: Saliwanchik, David R
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY:
                              APPLICATION NUMBER: US 07/342,212 FILING DATE: 21-APR-1992 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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GY: linear
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Pred. No. 20;
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; MOLECULE TYPE: protein US-08-356-405-2
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Best Local (
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                                                                                                     TELEFAX: (610)454-380 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: WO POFILING DATE: 29-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hen, Rene
APPLICANT: Plassat, Jean-Luc
TITLE OF INVENTION: Polypepti
TITLE OF INVENTION: Activity
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LENGTH: 75 amino acids
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TELEPHONE: 904-375-8100
                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                     APPLICATION NUMBER: FR 9:
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                 TYPE: ami
TOPOLOGY:
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                                                                                                                                                                                       NAME: Smith, Julie K REGISTRATION NUMBER:
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                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/356,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19426-0107
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                                                                                                                                   TELEPHONE:
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                                                                                                                     (610)454-3808
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Boschert, Ursula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhone-Poulenc Rorer Inc.
                                                                                                                                       (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides Having Serotonin Receptor Activity (5HT5A), Nucleic Acids Coding for These Polypeptides and Uses Thereof
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83.3%;
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Pred. No. 20;
1; Mismatches
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Best Local Similarity
"---hes 6; Conserv:
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Best Local Similarity
Fighter than 5; Conserv
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                                        Sequence 4, Application US/08969815 Patent No. 6207412
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                            GENERAL INFORMATION:
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APPLICANT: Sathe, Ganesh
APPLICANT: Van Horn, Ste
                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                             NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
CONTRACTOR NUMBER: US/08/806,263
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
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                                                                                                                            332 SRDTEEL 338
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CITY: King of Prussia
                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 24-FEB-1997
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                                                                                                                                                                                                                                                                                                                       371 amino acids
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Witte, Owen N. Weng, Zhigang
                                                                                                                                                                                  Conservative
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cDNA Clone HDPBI30 That Encodes
A No. 6221627el Human 7-Transmembrane Receptor
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75.0%;
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Pred. No.
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Pred. No.
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Best Local Similarity
Thehes 6; Conserve
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; FRAGMENT TYPE:
US-08-969-815-4
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NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: UCLA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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APPLICATION NUMBER: US/OR // CLASCT- US/OR // CL
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weng, Zhigang.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: TRANSCRIPTIONALLY REGULATED G PROTEIN-COUPLED
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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                                                                                                                                                                             COUNTRY: U.
ZIP: 92660
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                   CITY: Newport Beach STATE: CA
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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85.7%;
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Pred. No.
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ATTORNEY/AGENT INFORMATION:

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WAID, LAILY LAPPLICANT: WAILVINSON, DAVID
TITLE OF INVENTION: AND USE THEREOF
TITLE OF INVENTION: AND USE THEREOF
TITLE OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: lin
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bartfeld, Neil S
REGISTAGN NUMBER: 39,901
REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                         PRIOR APPLICATION DATA:
                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/969,815
FILING DATE: 13-NOV-1997
                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 SRDTEEL 347
                                                                                                                                             FILING DATE: 18-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
                                               APPLICATION NUMBER: FILING DATE: 12-DE
                                                                                                                                                                          APPLICATION NUMBER: US/08/167,919A
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                 APPLICATION NUMBER:
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5. 5674691
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internal
                                               12-DEC-1991
19-JUN-1992
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85.7%;
                                                             PK9992 (AU)
                 PCT/AU92/00294
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2e+02;
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US-08-715-106-11
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Best Local Similarity
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TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                            APPLICATION NUMBER: 08/167
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                            APPLICATION NUMBER: I
FILING DATE: 12-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOF
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
                REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 SRDDEVL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (516) 742-4366
TELEFAX: (516) 742-4366
TELEFAX: 730 901 SANS UR
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Garden City
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                                                            DiGiglio, Frank S.
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linear
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(516)
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85.78;
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                                                                                                                                                                PK9992 (AU)
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Pred. No. 2.3e+02;
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TELEFAX:

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MOLECULE TYPE: protein
US-08-715-106-11
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                                                                                                                                                                                                Sequence 12, Application Patent No. 6346406
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/150,440
CURRENT FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 465
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zalkin, Howard
APPLICANT: Smith, Janet L.
APPLICANT: Switzer, Robert L.
APPLICANT: Switzer, Robert L.
TITLE OF INVENTION: DEREGULATION OF GLUTAMINE PRPP AMIDOTRANSFERASE
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 3220-60979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Bacillus subtilis
PUBLICATION INFORMATION:
AUTHORS: Makaroff, Christopher
AUTHORS: Zalkin, Howard
                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: Switzer, Robert L.
AUTHORS: Vollmer, Steven J.
TITLE: Cloning of the Bacillis Subtilis Glutamine
TITLE: Phosphoribosylpyrophosphate Amidotransferase Gene
TITLE: Escherichia Coli
                                                                                                                                                                                                                                                                                                            ISSUE: 17
PAGES: 10586-10593
DATE: 1983-09-10
                                                                                                                                                                                                                                                                                                                                                          JOURNAL: J.
VOLUME: 258
              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                          125
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STRANDEDNESS: sir
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                                                                                                                                                          SSDTEVL 131
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                                                                             Application US/08914999
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              Ryazanov, Alexey G.
Hait, William N.
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Pavur, Karen S
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85.78;
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85.7%;
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Pred. No. 2.3e+02;
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Pred. No.
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2.5e+02;
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Best Local Similarity
Thehes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM:
US-08-914-999-12
                                                                                                                                                                                                                                                                                                                        Sequence 10
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   APPLICANT: Ryazanov, Alexey
APPLICANT: Hait, William N.
APPLICANT: Pavur, Karen S.
TITLE OF INVENTION: ELONGAT
TITLE OF INVENTION: AND MET
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: //
TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prot
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                    476 QTRDTE 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 411 Hackensack Ave, Continental Plaza, STREET: Floor
                                                                                                             CITY: Hackensack
STATE: New Jersey
                                                                                                                                            STREET: 411 Ha
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STATE: New Jersey
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                                                                                                                                                           411 Hackensack Ave, Continental Plaza, 4th
                                                                                                 USA
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Hait, William N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. elegans
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                           David A. Jackson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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AND METHODS OF USE THEREFOR
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Pred. No. 4.3e+02;
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CURRENT APPLICATION NUMBER: US/08/914,999

FILING DATE:
CLASSIFICATION: 435

ATTOREY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 601-1-078

TELEPONUMINICATION HORDRAFICO:
REFERENCE/DOCKET NUMBER: 601-1-078

TELEPONUM: 201-43-164

INFORMATION FOR SEQ ID NO. 10:
SEQUENCE CHARACITENISTICS:
LENGTH: 768 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORGANISM: C. elegans
US-08-914-99-10

OUGHNAME: 21.1%: Score 27: DB 4: Length 768:
Best Local Similarity 83.3%: Pred. No. 4.4e+02:
Matches 5: Conservative 1: Mismatches 0; Indels 0; Gaps

Oy 1 OSROTE 6

Db 476 OTROTE 481

Search completed: August 31, 2002, 12:15:45

Job time: 141 sec
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Result
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8: sp_organel1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
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Compugen Ltd
                  O9npr5 homo sapien Q15255 homo sapien Q15255 homo sapien O9d0h7 mus musculu o60140 schizosacch O9szz6 arabidopsis O97qa6 streptococc O9bak0 lepidothamn Q3236 tradescanti Q9bct8 homo sapien O9w2r1 drosophila Q9hct8 homo sapien O9l404 xenopus lae Q46025 corynebacte Q90m04 human immun
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## ALIGNMENTS

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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  human gene transcripts.";
Submitted (JUN-2000) to the EMEMEL; AL359057; CAB94390.1; -.
InterPro: IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 2.
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NON_TER
SEQUENCE
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Q9NPR5;
01-OCT-2000 (TrembLrel. 15, Created)
01-OCT-2000 (TrembLrel. 15, Last sequence update)
01-JUN-2001 (TrembLrel. 17, Last annotation update)
PTPRJ, PROTEIN TYROSINE PHOSPHATASE RECEPTOR J, ETA
Homo sapiens (Human).
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Andreu N., Estivill X.,
Submitted (JUN-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Auffray C., Ansorge W., Ballab
Lehrach H., Poustka A., Lundebe
"The European IMAGE consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
324 QSRDTEVL
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Lundeberg J.
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                                                                                                                                 0;
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Pred. No. 1.3;
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databases
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EMBL; D37781; BAA07035.1; -.
HSSP; P18052; 1YFO.
InterPro; IPR001395; Aldo_ket_red.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00041; fn3; 5.
Pfam; PF00102; Y_phosphatase; 1.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-EMBRYO;

STRAIN-C57BL/6J; TISSUE-EMBRYO;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-2108560; PubMed-11217851;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii '
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Sait
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9D0H7 PRELIMINARY;
Q9D0H7;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
2610016F07RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q15255 PRELIMINARY; PRT; 1337 AA. Q15255; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PROTEIN-TYROSINE PHOSPHATASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSIT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00063; ALDOKETO_REDUCTASE_3; PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1 PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
SIGNAL
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Honda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSRDTEVL 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Transit peptide.
19 38 POTENTIAL.
971 995 POTENTIAL.
1337 AA; 145802 MW; BA7EA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Primates;
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Catarrhini;
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Peta.";
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RESULT
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Best Local S
Matches 7
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Best Local Similarity
Matches 6; Conser
             Q9SZZ6

Q9SZZ6;
Q9SZZ6;
Q1-MAY-2000 (TrEMBLrel. 13, Creation Coresion CTEMBLrel. 15, Last O1-OCT-2000 (TrEMBLrel. 15, Last O1-OCT-2000 (TrEMBLrel. 15, Last HYPOTHETICAL 27,8 KDA PROTEIN. L73G19.60 OR Ar4G25680.

L73G19.60 OR Ar4G25680.

Arabidopsis thaliana (Mouse-ear Friedrich Visialiana (Mouse-ear Friedrich Visiali
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060140;
01-AUG-1998
01-AUG-1998
01-OCT-2000
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01-AUG-1998 (TREMBLrel. 07, Last sequence update)
01-OCT-2000 (TREMBLrel. 15, Last annotation update)
HYPOTHETICAL 49.1 KDA PROTEIN.
SPBC18H10.09.
SCHIZOSACCHAROMYCES pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyne M., Rajandream M.A., Ba Submitted (MAR-1998) to the EMBL; AL022304; CAA18406.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 42
  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
EMBL; AK011417; BAB27605.1; -.
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Kuehl P., L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
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Lewis S., Matsuo Y., J
  Viridiplantae;
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428 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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ne EMBL/GenBank/DDBJ c
se-ear cress).
Streptophyta;
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                                                                                     Last sequence update)
Last annotation update)
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Pred.
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Pred. No.
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Nikaido I., Pesc
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam I.A., White O., Salzberg S.L., Lewis M.R., Radune D., Umayam I.A., White N., Molf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey I Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q970A6;
01-OCT-2001 (TremBLrel. 18,
01-OCT-2001 (TremBLrel. 18,
01-DEC-2001 (TremBLrel. 19,
V-TYPE SODIUM ATP SYNTHASE,
                                                                                                                      Complete
SEQUENCE
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Submitted (MAR-2000) to the EMBL/G
EMBL; AL050400; CAB43599.1; -
EMBL; AL151563; CAB81378.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bevan M., Pohl T., Weizenegger T., Mayer K.F.X., Schueller C.; Submitted (MAY-1999) to the EMBL/G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
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                                                                                                                                                                   TIGR; SP1319;
                                                                                                                                                                                      Science 293:498-506(2001).
EMBL; AE007430; AAK75417.1;
                                                                                                                                                                                                                                   pneumoniae
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    Similarity 6; Conserv
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Score 31; DB:
Pred. No. 46;
1; Mismatches
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SUBUNIT C.
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RI Aust. Syst. Bot. 0:0-0(2000).

C: FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-1: FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-1: FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE PHOTOSYNTHETIC CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME CC ACTIVE SITE (BY SIMILARITY).

CC -1: CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-CC PHOSPHO-D-GLYCERATE.

CC PHOSPHO-D-GLYCERATE + 2-PHOSPHOSPHATE + O(2) = 3-CC PHOSPHO-D-GLYCERATE + 2-PHOSPHOSPHATE + O(2) = 3-CC SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).

CC -1: SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).

CR EMBL; AF249642: AAK29524.1; -.

DR HSSP; D04718; TRUS.

R HSSP; D04718; RUBISCO_large.

DR HSSP; D04718; RUBISCO_large.
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01-JUN-2001
01-JUN-2001
01-NOV-1996 (TrEMBLrel. 01, Create 01-NOV-1996 (TrEMBLrel. 11, Last s 01-DEC-2001 (TREMBLREl. 19, Last a RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE SUBUNIT) (FRAGMENT).
                                                                                                                                                                                          Q33236
Q33236;
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SEQUENCE
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Pfam; PF02788; RuBisCO_large_N; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
Carbon dioxide fixation; Chloroplast; Lyase; Mono Oxido_reductase; Photorespiration; Photosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Generic relationships within and between the Podocarpaceae and Phyllocladaceae based on an
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
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446 AA;
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Coniferopsida; Coniferales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446
49394
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                                  Last sequence update)
Last annotation updat
XYLASE LARGE CHAIN (EC
                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31;
Pred. No.
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62;
                                      tion update)
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es; Podocarpaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 446;
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                                          4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT
Q95CG3
DT DT Q95CG3
OC Q9
OC 
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Q95CG3
Q95CG3;
JT 01-DEC-2001 (TrEMBLrel. 19, Last sc.,
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotati
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotati
TTRUIOSE 1,5-BISPHOSPHATE CARBOXYLASE LAI
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Best Local S
Matches 5
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Lubmitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.

C -I- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-

RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC

CRABON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF

THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH

C REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME

ACTIVE SITE (BY SIMILARITY).

C -I- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-

C PHOSPHO-D-GLYCERATE + Z-PHOSPHOGLYCOLATE.

C -I- SUBGELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
SEQUENCE
                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00016; RuBisCO_large; 1.
Pfam; PF02788; RuBisCO_large_N; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis.
                                                                                                                                 Chloroplast.
                                                                                                                                                                     EMBL; AF312238; AAL26157.1;
                                                                                                                                                                                                      Analysis of rbcL Sequence Da
Submitted (OCT-2000) to the
                                                                                                                                                                                                                               Byans T.M., Faden R.B., Givnish the "Phylogenetic Relationships in the "Phylogenetic Relationships in the "Phylogenetic Relationships in the "Phylogenetic Relationships" in t
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tradescantia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00016; RuBisCO_large;
Pfam; PF02788; RuBisCO_large_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: CHLOROPLAST (-i- SIMILARITY: BELONGS TO THE RUBISCO EMBL; L05463; AAA98393.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith J.F., Kress W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta;
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                            456
50570 MW;
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zimmer E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptophyta; Embryophyta; Tracheophyta;
/ta; Liliopsida; Commelinales; Commelinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB Pred. No. 63; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
ARBOXYLASE LARGE SUBUNIT (FRAGMENT).
                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liliopsida;
                            13477E0E231F0440 CRC64;
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                                                                                                                                                                                                                                                                                                          Т.Ј.,
                                                                                                                                                                                                                                                                          J., Sytsma K.J.;
Commelinaceae:
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a; Commelinales; Commelinac
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                                                                                                                                                                                                                                                                                                          K.J.;
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                                                                                                                                                                                                                                                                              II.
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RY SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RY STRAIN-BERKELEY;

RX MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,

RA Abril G., Rogers R., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Pallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Pallew R.M., Basu A., Bareman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                RESULT
                     Q9нст8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                               Eukaryota; |
Pterygota;
                                                                                                                                                                                                                                                                                 01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                         CG9993
CG9993.
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                   Q9W2R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear hormone receptor transcriptional coactivator. Mol. Cell. Biol. 20:6138-6146(2000). EMBL; AF280094; AAF99318.; -...
Interpro; IPR000770; SAND.
SMART; SM00258; SAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U1-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, TRANSCRIPTIONAL COACTIVATOR HOMO SERVICES (""----")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloch D.B., Nakajima A., Gulick T., Chiche J.D., Orth D., de La Monte S.M., Bloch K.D.; "Spil0 localizes to the PML-Spi00 nuclear body and may function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).

Metazoa; Chordata;
                                                                                                                                                                                                      Ephydroidea;
                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                        Q9W2R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                        NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
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                                                                                                                                                                                                                                                                      PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6;
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0 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                    Neoptera; Endopterygota; Diptera;
prosophilidae; Drosophila.
                                                                                                                                                                                                                               Metazoa; Arthropoda; Tracheata; Hexapoda;
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed-10913195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.6%;
75.0%;
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                                                                                                                                                                                                                                                                                    13,
13,
                                                                                                                                                                                                                                          (Fruit fly).
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                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
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SP110B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4EBA8F7FF90D1CB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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No.
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                                                                                                                                                                                                                                                                                                                                      543 AA
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76;
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                                                                                                                                                                                                                   Brachycera; Muscomorpha;
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RESULT
Q9Ha58
ID Q9
AC Q9
DT Q1
DT Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 6
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP280095; AAG09826.1; ~. InterPro; IPR001487; Bromodomain.

InterPro; IPR001965; PHD.

InterPro; IPR000770; SAND.
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                          Bloch D.B., Nakajima A., de la Monte S.M., Bloch I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSCRIPTIONAL COACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9нв58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HB58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burtis K.C., Busam D.A.,
Cherry J.M., Cawley S., J
de Pablos B., Delcher A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burtis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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HSSP, P08659; ILCI:
FlyBase; FBgn0034553; CG9993.
InterPro; IPR0000873; AMP-bind.
InterPro; IPR000508; Peptidase_S26.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00761; SPASE_I_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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mes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.R., Bouck J., Brokstein P., Brottier P.
D.A., Butler H., Cadieu E., Center A., Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
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Last sequence update)
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Sp110.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vo
Catarrhini;
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77;
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Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          v B.C., Dunn P.,
Fleischmann W.,
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Smith H.O.,
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Best Local
                                                                                                                                                                                                                                                                                                01-NOV-1996
01-NOV-1996
01-JUN-2001
Tai S.S., Zhu Y.Y.;
"Cloning of a Corynebacterium diphtheriae iron-repressible gene that hares sequence homology with the AhpC subunit of alkyl hydroperoxide
                                                                                                                                                                                                                                                                                                                                                            Q46025
Q46025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-95290499; PubMed-7772598;

Adati N., Ito T., Koya C., Kito K., Sakaki Y., Shiokawa K.;

"Differential display analysis of gene expression in develor

"Differe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91404
Q91404;
                                                                                                                                                    Actinomycetales;
Corynebacterium.
NCBI_TaxID=1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
Amphibia; Batrachia; Anura; Mesobatrach
                                                                                                                                                                                                                  Corynebacterium diphtheriae. Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                            DIRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00226; IF; 1. Coiled coil; Intermediate filament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S78089; AAB34522.1; -.
InterPro; IPR001664; IF.
Pfam; PF00038; fflament; 1.
PROSITE; PS00226; IF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                     MEDLINE-95286547; PubMed-7768861; Tai S.S., Zhu Y.Y.;
                                                                                               STRAIN=C7
                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                             IRON REPRESSIBLE POLYPEPTIDE.
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expression in developing
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ia; Pipoidea; Pipidae;
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RESULT 15

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ID Q90M04;
AC Q90M04;
DT 01-DEC-2001 (TIEMBLrel. 19, Created)
DT 01-DEC-2001 (TIEMBLREL 19, Last sequence update)
DT 01-DEC-2001 (TIEMBLREL 19, Last sequence update)
DT 01-DEC-2001 (TIEMBLREL 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WM1014;
RA Herring B.L., Dwyer D.E.;
RI "Australian HIV-1 env subtypes.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF400083; AAK91742.1; -.

FT NON_TER 218 218
SQUENCE 218 AA; 24303 MW; E8F49BA240566450 CRC64;
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Search completed: August 31, Job time: 219 sec
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Herring B.L., Dwyer D.E.;
"Australian HIV-1 env subtypes.";
submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF400083; AAK91742.1; -.
NON_TER 1 1
NON_TER 218 218
NON_TER 218 AA; 24303 MW; E8F49BA240566450 CRC64;
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J. Bacteriol. 177.3512-3517(1995).

EMBL; U18620; AAA96946.1; -.

Interpro; IPR000866; AhpC-TSA.

Pfam; PF00578; AhpC-TSA; 1.

SEQUENCE 198 AA; 22312 MW; 7A09DCB4A07705DD CRC64;
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198 ESRDTEI 204
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76 QDRDTQIL 83
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24303 MW; E8F49BA240566450 CRC64;
                                                                                                                                                                           78.9%; Score 30; DB 15; Length 218; 71.4%; Pred. No. 50; tive 2; Mismatches 0; Indels
                      2002, 12:19:09
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2; Mismatches
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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	P92406 P48606 Q32026 Q32026 P28426 P28426 P28426 Q31859 Q31951 Q31951 Q32698	RBL_NOLSP

## ALIGNMENTS

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RESULT 1
PTPJ_HUMAN
                   InterPro; IPR00
InterPro; IPR00
Pfam; PF00041;
                                                                                           EMBL; U10886;
EMBL; D37781;
HSSP; P18052;
MIM; 600925; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-95024024; PubMed-7937872;
Oestman A., Yang Q., Tonks N.K.;
"Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced with increasing cell density.";
Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-95086212; PubMed-7994032; Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.; "Molecular cloning, Characterization, and chromosomal localization can novel protein-tyrosine phosphatase, HPTP eta."; Blood 84:4186-4194(1994).

-I-- EUNCTION: MAY CONTRIBUTE TO THE MECHANISM OF CONTACT INHIBITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTPJ_HUMAN STANDARD; PRT; 1337 AA. Q12913; Q15255; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                  -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = pr
tyrosine + phosphate.
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- PTM: N- AND O-GLYCOSYLATED.
-I- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
-I- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- DATABASE: NAME=PROW; NOTE=CD guide CD148 entry;
WMW="http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                     InterPro; IPR003961; FN_III.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00041; fn3; 5.
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PF00102; Y_phosphatase; 1.
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                                                                                                                                AAB36687.1;
BAA07035.1;
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RESULT 2
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AC 060179;
DT 16-OCT-2001 0
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MEDLINE-98196666; PubMed-9537320;

Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenv
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;

Feldman R.A., Short J.M., Obserthermophilic bacterium
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Bacteria; Aquificales;
NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical 186.4 kDa protein C23E6.04c in c SPBC23E6.04C.
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REPEAT 1608 16
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PROSITE; PS50077; HEAT_REPEAT; 1.
                                                                                                                -!- SIMILARITY: TO A.AEOLICUS
                                                                                                                                          Nature 392:353-358(1998)
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                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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al protein AQ_1211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1646
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85.7%;
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                                                                                                                                                                                                                                                                                                      Aquificaceae; Aquifex
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                                                                                                                                                                                                                                                                                                                                                            sequence update)
annotation update)
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Pred. No. 71;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAT
                                                                                                                         AQ_820 AND AQ_1583.
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                                                                                                                                                                                                                                                                                                                                                                                                                     203 AA
                         (See http://www.isb-sib
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RESULT 4
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Hypothetical
SEQUENCE 20
                                                                                                                                                                                Prodm; PF00275; EPSP_Syntase; 1.
Prodom; PB001867; EPSP_SYntase; 1.
PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
Aromatic amino acid biosynthesis; Transferase; CSEQUENCE 430 AA; 44557 MW; 445975BA53DC74D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N. Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AROA_MYCLE STANDARD; PRT; 430 AA. 09CCI3; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 3-phosphoshikimate 1-carboxyvinyltransferase (EC enolpyruvylshikimate-3-phosphate synthase) (EPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions used by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-i- CATALYTIC ACTIVITY: Phosphoenolpyruvate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001986; EPSP_syntase. Pfam; PF00275; EPSP_syntase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21128732; PubMed=11234002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Leproma; ML0792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate. PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHW SUBUNIT: MONOMER (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
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QKRDSEVL 78
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Score 29; DB Pred. No. 43; 3; Mismatches
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Pred. No. 11;
1; Mismatches
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BFCCE047E973AF29 CRC64;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
             EMBL;
                                                                                                                                                                                                                        laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
-!- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHY SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC enolpyruvylshikimate-3-phosphate synthase) (EPSP AROA OR RV3227 OR MT3324 OR MTCY20B11.02.
                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91072223; PubMed=2123856; Garbe T., Jones C., Charles I.G., Dougland and characterization of the tuberculosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
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01-AUG-1991
                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98295987; PubMed=9634230;
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                                                                                                                                                                                                                                                                                                                                        "Whole genome comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol.
                                                                                                                                                                                          SUBCELLULAR SIMILARITY:
                                                                                                                           European Bioinformatics Institute.
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X52269;
M62708;
Z95121;
; CAA36510.1;
; AAA25356.1;
; CAB08328.1;
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THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
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the aroA gen
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DF_CANE,
DF_CANEA,
C CDF_CANFA,
C Q29473; 002859;
T 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update,
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DT 15-chrome P450 2D15 (EC 1.14.14.1) (CYPIID15) (P4
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                                               MEDLINE-98162950; run....Ttoh S., Oha Tasaki T., Nakamura A., Itoh S., Oha Tasaki T., Kazusaka A., Kamataki T., Iwata H., Kazusaka A., Kamataki Oharacterization of
                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00275; EBSP_Syntase; 1.
ProDom; PD001867; EPSP_Syntase; 1.
PROSITE; PS00104; EPSP_SYNTHASE; 1.
PROSITE; PS00104; EPSP_SYNTHASE_2; 1.
Aromatic amino acid biosynthesis; Transferase; Complete SEQUENCE 450 AA; 46425 MW; 27BB86F9412A07D5 CRC64;
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PIR;
           the
                                                                                                                                                                CHARACTERIZATION.
MEDLINE-98389575; PubMed-9721180;
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characterization.";
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InterPro; IPR001986; EPSP_syntase.
                                                                                                                          "Expression and characterization of canine Arch. Biochem. Biophys. 357:27-36(1998).
                                                                                                                                                Tweedie
                                                                                                                                                                                                          expression
                                                                                                                                                                                                                                              MEDLINE-98162950; PubMed-9504424;
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                                                                                                                                                                                                                                                                                                                                             Sakamoto
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
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Takanaka A., Matsubara
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                                                                                                                                                                                                 Biochem.
                                                                                                                                                                                                                                                                                                                        new cytochrome P450
         s SWISS-PROT entry is copyright. It is produced through a collaboratio ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
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A37807; A37
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5; Conser
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A37807.
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62.5%;
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Pred. No. 45;
3; Mismatches
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; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                             cloning,
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T., Fujita S.;
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pean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/

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CPDG_CAVPO
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                                                                                                                                                                                                                                                                                                            STRAIN-HARTLEY WHITE; TISSUE-Adrenal gland;
STRAIN-HARTLEY WHITE; TISSUE-Adrenal gland;
Sun Y., Volgt J.M., Pierce J.C., Colby H.D.;
"The gene sequence of a xenobiotic metabolism-related cytochrome
"The gene sequence of a xenobiotic metabolism-related cytochrome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome P450 2D16 (EC 1.14.14.1) (CYPIID
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPDG_CAVPC
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and sequencing of a guinea pig cytochrome P4502D (CYP2D16): high level expression in adrenal microsomes."; Biochem. Biophys. Res. Commun. 209:1149-1156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jiang Q., Voigt J.M., Colby H.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=13; TISSUE=Adrenal cortex;
MEDLINE=95251703; PubMed=7733969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10141;
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INIT_MET
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                                                                      ACIDS, AND XENOBIOTICS.

CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) - Oxidized flavoprotein + H(2)O.

SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic retic TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE INN THE ADRENAL CORTEX.

SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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6; Conser
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56301 MW;
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Rodentia;
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Pred.
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; 27E352B5B309E7F1 CRC64;
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Hystricognathi; Caviidae; Cavia.
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(CYPIID16).
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                         outstation
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Matches 6
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Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086
                                                                                                                                                                                                                                                             Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

-i- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is possible that it carries out the mismatch recognition step. This protein has a weak ATPase activity (By similarity).

-i- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                         InterPro; IPR000432; MutS_C.
InterPro; IPR002863; MutS_N.
Pfam; PF00488; MutS_C; 1.
Pfam; PF016624; MutS_N; 1.
ProDom; PD001263; MutS_C; 1.
                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99XL8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA mismatch repair MUTS OR SPY2148.
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Microsome; Endoplasmic reticulum.
                               SMART; SM00534; MUTSac; 1
SMART; SM00533; MUTSd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21192684; PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTS_STRPY
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                   PROSITE;
                                                                                                                                  EMBL; AE006633; AAK34785.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382
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PS00486; DNA_MISMATCH_REPAIR_2; 1.
ir; ATP-binding; DNA-binding; Complete proteome
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446
123
127
                                                                                                                                                                                                                                                                                                                                                                                                                                            700294 / SEROTYPE M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein muts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55800 MW;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEME (BY SIMILARITY).
I -> V (IN REF. 2).
Y -> N (IN REF. 2).
G -> R (IN REF. 2).
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electron transport; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2429247E49BF6B24 CRC64;
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                                                                                                                                                                                                   There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
51;
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MBL outstation -
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ANK2_HUMAN
ID ANK2_H
AC Q01484
DT 01-APR
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DT 16-OCT
DE Ankyri
GN ANK2.
OS Homo s
OC Eukary
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Best Local
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Q01484; Q01485;
01-APR-1993 (Rel. 2
01-OCT-1996 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                    1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maurer K.C.T., Urbanus J.H.M., Planta R.J.;
"Sequence analysis of a 30 kb DNA segment from yeast che carrying a ribosomal protein gene cluster, the genes er plasma membrane protein and a subunit of replication for novel putative serine/threonine protein kinase gene.";

Yeast 11:1303-1310(1995).

-I- SIMILARITY: SOME, TO S.POMBE SPAC23D3.13C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YN37_YEAST STANDARD; PRT; 1636 AA. P48563; Created) 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update Hypothetical 186.8 kDa protein in CLA4-PUS4 YNL297C OR N0453.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                        Ankyrin
                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 1636 AA;
                                                                                                                                                                                                                                                                                                            SGD;
                                                                                                                                                                                                                                                                                                                      EMBL; U23084; AAC49101.1; -. EMBL; 271573; CAA96214.1; -.
                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as modified and this statement is not removed. Use this requires a license agreement (See htter)
                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96132033; PubMed=8553702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                            S0005241; YNL297C.
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851 AA;
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                                                                                                                                                                                                                      Conservative
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                                                                                                     STANDARD;
                            25, Created)
34, Last sequence update)
40, Last annotation update)
. 40, Ankyrin B) (Ankyrin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33, Created)33, Last sequence update)39, Last annotation update)
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Pred. No.
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; 737D51CBCDFEAF0A CRC64;
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95;
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                                         nonerythroid)
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n factor C, a
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PRINTS; PRO1415; ANKYRIN.
SMART; SM00248; ANK; 21.
SMART; SM00005; DEATH; 1.
SMART; SM00218; ZU5; 1.
SMART; SM00218; ANK_REPEAT; 20.
PROSITE; PS50088; ANK_REP_REGION; 1
PROSITE; PS50297; ANK_REP_REGION; 1
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X56957; CAA40278.1; -. EMBL; X56958; CAA40279.2; -. EMBL; Z26634; CAB42644.1; -. EMBL; M37123; AAA62828.1; -. PIR; S14533; S14533. PIR; A39643; A39643.
                                                                                                                                                                 InterPro;
Pfam; PFO;
Pfam; PFO;
Pfam; PFO;
                                                                                                                                                                                                                                                                                                            MIM;
                                                                                                                                                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Attach integral membrane proteins to cytoskeletal elements. Also bind to cytoskeletal proteins.
-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL CELLS THROUGHOUT THE BRAIN.
-!- PTM: PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN EACH PHOSPHORYLATION EVENT PHOSPHORYLATION EVENT PHOSPHORYLATION EVENT PHOSPHORYLATION EVENT 
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MEDLINE=92009921; PubMed=183308;
MEDENTS WENT:, Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-Brain stem;
MEDLINE-91302466; PubMed-1830053;
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDNAs encoding ankyrins reveal a family of alternatively spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-94075409; PubMed-8253844;
Chan W., Kordeli E., Bennett V.;
"440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyelinated axons.";
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                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND FUNCTION (POTENTIAL).
SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                       B39643; B39643.
S14569; S14569.
                                                                                                                                                                     PF00791;
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                                                                                                                                                                                                                                                                                                                               Q00421; 1AWC
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                Hypothetical C12L.
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                                                                           RSRDVEVL 1343
                                                                                                Similarity 75.6; Conservative
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                                     (Rel. 27, Created)
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     viruses,
           (strain Kasza)
                                                STANDARD;
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      no
                           sequence update) annotation updat
      RNA stage;
                                                                                                                          QY -> HA (IN REF. 1).
I -> Y (IN REF. 1).
MW; 52AC496C428E29D2
                                                                                                1;
                                                                                                Score 29; DB
Pred. No. 5.6e
1; Mismatches
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GQ -> PE
I -> S (
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      Poxviridae; Chordopoxvirinae;
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PDXJ_SYNY3 STANDARD; PRT; 2
P72776;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                             between
the Euro
              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            This
                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions." DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                 Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamu Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T. Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., C Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strai
Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDXJ OR SLR1779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massung R.F., Jayarama V., Moyer R.W.;
"DNA sequence analysis of conserved and unique regions of swinepox virus: identification of genetic elements supporting phenotypic observations including a novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                       Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1148;
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[1]
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                                                                          s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                   PYRIDOXAL PHOSPHATE.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE PDXJ FAMILY.
                                                                                                                                                                                      FUNCTION: CATALYZES THE CONDENSATION OF 1-DEOXY-D-XYLULOSE-5-PHOSPHATE (DXY) AND 1-AMINO-3-OXO-4-(PHOSPHOTEXTY) PROPAN-2-ONE TO FORM PRILOXINE 5'-PHOSPHATE (PNP) (BY SIMILARITY).

PATHWAY: DE NOVO SYNTHESIS OF PYRIDOXINE (VITAMIN B6) AND
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
5 AA; 9174 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biosynthetic protein
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P47694; Q49238;
01-FEB-1996 (Rel. 3
01-FEB-1996 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                     EMBL; U39727; PEMBL; U39732; PEMBL; U01790; PEMBL; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser C.M., Cocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (some send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 175:7918-7930(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 86-182 FROM N.A. STRAIN=ATCC 33530 / G-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-ATCC 33530 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A survey of the Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peterson S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94075230;
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; AAD10612.1;
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                                                                                                         AA;
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Hu P.-C., Bott K.F.,
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62.
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D142C358CE474C71 CRC64;
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by using random
                                         Length 334;
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RESULT 15
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HA19_CANFA
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InterPro; IPROULL.
InterPro; IPROULL.
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P18466;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence upda
15-JUL-1999 (Rel. 38, Last annotation up
DLA class I histocompatibility antigen,
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-i- FUNCTION: INVOLVED IN THE PRESENTATION
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EXTRACELLULAR ALPHA-1.
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EXTRACELLULAR ALPHA-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                      Pfam; PF02788; RuBisCO_large_N; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Phylogenetics of seed plants: an analysis of nucleotide sequences from the plastid gene rbcL.";
Ann. Mo. Bot. Gard. 80:528-580(1993).
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01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ribulose bisphosphate carboxylase large chain
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phospho-D-glycerate.
CATALYTIC ACTIVIT: D-RIBULOSE 1,5-BISPHOSPHATE +
3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHAFE, THE PRIMARY EVENT IN PHOTOSYMTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION (THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY:
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QSRDTEVL
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                                                                        Similarity
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IPR000685; RuBisCO_large.
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Magnoliophyta; Liliopsida; Alismataceae; Alisma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               license agreement (See http://www.isb-sib.ch/announce/
                                                                      73.7%;
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